OM protein - protein search, using sw model

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Run on: February 23, 2005, 19:23:02 ; Search time 30.1695 seconds
(without alignments)
220.215 Million cell updates/sec

Title: US-09-267-511-3
Perfect score: 120
Sequence: 1 XXXXXXXXXXXXXXXXXXXXX..........XXXXXXXXXXXXXXXX 89
Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents AA.*
   1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
   2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
   3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
   4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
   5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
   6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40	33.3	9	3	US-08-324-297A-2	Sequence 2, Appli
2	40	33.3	9	4	US-09-187-330-5	Sequence 5, Appli
3	40	33.3	9	4	US-09-187-330-36	Sequence 36, Appl
4	40	33.3	10	3	US-08-324-297A-3	Sequence 3, Appli
5	40	33.3	10	4	US-08-324-297A-16	Sequence 16, Appl
6	40	33.3	11	4	US-08-324-297A-16	Sequence 22, Appl
7	40	33.3	14	1	US-07-871-973A-2	Sequence 2, Appl
8	40	33.3	14	3	US-08-324-297A-1	Sequence 1, Appli
9	40	33.3	14	3	US-08-324-297A-23	Sequence 23, Appl
10	40	33.3	15	4	US-09-187-330-21	Sequence 21, Appli
11	40	33.3	15	4	US-09-187-330-23	Sequence 23, Appl
12	40	33.3	19	1	US-08-379-613-5	Sequence 5, Appl
13	36	30.0	24	3	US-08-324-297A-5	Sequence 5, Appli
14	34	28.3	9	4	US-09-248-796A-19008	Sequence 19008, A
15	33	27.5	409	4	US-09-248-796A-7	Sequence 7, Appli
16	32	26.7	24	3	US-08-860-300-2	Sequence 2, Appli
17	32	26.7	24	5	PCT-US95-16596-2	Sequence 2, Appli
18	32	26.7	193	4	US-09-438-185A-222	Sequence 222, App
19	31	25.8	14	3	US-08-324-297A-14	Sequence 14, Appl
20	31	25.8	14	4	US-09-187-330-24	Sequence 24, Appl
21	31	25.8	24	2	US-08-706-209-3	Sequence 3, Appli
22	31	25.8	24	2	US-08-706-209-4	Sequence 4, Appli
23	31	25.8	24	2	US-08-817-177-5	Sequence 5, Appli
24	31	25.8	24	3	US-08-706-209-4	Sequence 4, Appli
25	31	25.8	24	3	US-08-860-300-1	Sequence 1, Appli
26	31	25.8	24	3	US-08-860-300-3	Sequence 3, Appli
27	31	25.8	24	3	US-08-860-300-4	Sequence 4, Appli
28	31	25.8	24	3	US-08-860-300-5	Sequence 5, Appli
29	31	25.8	24	4	US-08-981-861-2	Sequence 2, Appli
30	31	25.8	24	5	PCT-US95-12686-5	Sequence 5, Appl
31	31	25.8	24	5	PCT-US95-16596-1	Sequence 1, Appli
32	31	25.8	24	5	PCT-US95-16596-3	Sequence 3, Appli
33	31	25.8	24	5	PCT-US95-16596-4	Sequence 4, Appli
34	31	25.8	24	5	PCT-US95-16596-5	Sequence 5, Appli
35	31	25.8	24	5	PCT-US96-11373-2	Sequence 2, Appli
36	31	25.8	24	2	US-08-467-822-35	Sequence 35, Appl
37	31	25.8	547	2	US-08-432-697-35	Sequence 35, Appl
38	31	25.8	547	3	US-08-466-248-35	Sequence 35, Appl
39	31	25.8	573	2	US-08-706-209-1	Sequence 1, Appli
40	31	25.8	573	3	US-08-981-787-1	Sequence 1, Appli
41	31	25.8	573	3	US-08-461-722-1	Sequence 1, Appli
42	31	25.8	573	3	US-08-336-251-1	Sequence 1, Appli
43	31	25.8	573	4	US-09-468-041-1	Sequence 1, Appli
44	31	25.8	573	4	US-08-981-861-1	Sequence 1, Appli
45	31	25.8	573	4	US-09-613-743A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-324-297A-2
Sequence 2, Application US/08324297A
Patent No. 6174862
GENERAL INFORMATION:
  APPLICANT: Brenneman, Douglas E.
  APPLICANT: Gozes, Illana
  TITLE OF INVENTION: Neurotrophic Peptides of Activity
  TITLE OF INVENTION: Dependent Neurotrophic Factor
  NUMBER OF SEQUENCES: 21
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew
    STREET: One Market Plaza, Steuart Street Tower
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94105-1492
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/324,297A
    FILING DATE: 17-OCT-1994
    CLASSIFICATION: 514
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/871,973
    FILING DATE: 22-APR-1992
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/688,087
    FILING DATE: 22-APR-1991
  ATTORNEY/AGENT INFORMATION:
    NAME: Garrett-Wackowski, Eugenia
    REGISTRATION NUMBER: 37,330
    REFERENCE/DOCKET NUMBER: 15280-178-1US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 543-9600
    TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 9 amino acids
    TYPE: amino acid
    STRANDEDNESS:
    TOPOLOGY: linear
  MOLECULE TYPE: peptide
US-08-324-297A-2

Query Match   33.3%; Score 40; DB 3; Length 9;
Best Local Similarity   100.0%; Pred. No. 4.1e+05;

Matches   9;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy      41 SALLRSIPA 49
           |||||||||
Db       1 SALLRSIPA 9
```

RESULT 2
US-09-187-330-5
Sequence 5, Application US/09187330
Patent No. 6613740
GENERAL INFORMATION:
APPLICANT: Gozes, Illana
APPLICANT: Brenneman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamostiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-29120US
CURRENT APPLICATION NUMBER: US/09/187,330
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/037,404
EARLIER FILING DATE: 1997-02-07
EARLIER APPLICATION NUMBER: WO PCT/US98/02485
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF-9 active
OTHER INFORMATION: peptide antigen

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Qy      41 SALLRSIPA 49
           |||||||||
Db       1 SALLRSIPA 9
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Query Match   33.3%;   Score 40;   DB 4;   Length 9;
Best Local Similarity   100.0%;   Pred. No. 4.1e+05;
Matches   9;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 3
US-09-187-330-36
Sequence 36, Application US/09187330
Patent No. 6613740
GENERAL INFORMATION:
APPLICANT: Gozes, Illana
APPLICANT: Brenneman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamostiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-29120US
CURRENT APPLICATION NUMBER: US/09/187,330
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/037,404
EARLIER FILING DATE: 1997-02-07
EARLIER APPLICATION NUMBER: WO PCT/US98/02485
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF-9 active
OTHER INFORMATION: peptide adsorbed onto bovine serum albumin (BSA)
OTHER INFORMATION: as antigen
US-09-187-330-36

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Qy      41 SALLRSIPA 49
           |||||||||
Db       1 SALLRSIPA 9
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RESULT 4
US-08-324-297A-3
Sequence 3, Application US/08324297A
Patent No. 6174862
GENERAL INFORMATION:
APPLICANT: Brenneman, Douglas E.
APPLICANT: Gozes, Illana
TITLE OF INVENTION: Neurotrophic Peptides of Activity
TITLE OF INVENTION: Dependent Neurotrophic Factor
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,297A
FILING DATE: 17-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,973
FILING DATE: 22-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,087
FILING DATE: 22-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-178-1US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-324-297A-3

Query Match   33.3%;   Score 40;   DB 3;   Length 10;
Best Local Similarity   100.0%;   Pred. No. 0.014;
Matches   9;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy      41 SALLRSIPA 49
           |||||||||
Db       2 SALLRSIPA 10
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RESULT 5

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US-09-187-330-22
Sequence 22, Application US/09187330
Patent No. 6613740
GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-2912000US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: conjugated through the Cys residue to Sephadex for
; OTHER INFORMATION: affinity chromatography

Query Match             33.3%;  Score 40;  DB 4;  Length 10;
Best Local Similarity   100.0%;  Pred. No. 0.014;
Matches    9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy         41 SALLRSIPA 49
              |||||||||
Db          2 SALLRSIPA 10


RESULT 6
US-08-324-297A-16
Sequence 16, Application US/08324297A
Patent No. 6174862
GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Gozes, Illana
; TITLE OF INVENTION: Neurotrophic Peptides of Activity
; TITLE OF INVENTION: Dependent Neurotrophic Factor
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,297A
; FILING DATE: 17-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/871,973
; FILING DATE: 22-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 514
; CLASSIFICATION: 514
; FILING DATE: 22-APR-1991
; APPLICATION NUMBER: US 07/688,087
; FILING DATE: 22-APR-1991
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 15280-178-1US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa = an amino acid
; OTHER INFORMATION: sequence comprising from 1 to about
; OTHER INFORMATION: 40 amino acids wherein each amino
; OTHER INFORMATION: acid is independently selected from
; OTHER INFORMATION: the group consisting of naturally
; OTHER INFORMATION: occurring amino acids and mimetics"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Xaa = an amino acid
; OTHER INFORMATION: sequence comprising from 1 to about
; OTHER INFORMATION: 40 amino acids wherein each amino
; OTHER INFORMATION: acid is independently selected from
; OTHER INFORMATION: the group consisting of naturally
; OTHER INFORMATION: occurring amino acids and mimetics"
US-08-324-297A-16

Query Match             33.3%;  Score 40;  DB 3;  Length 11;
Best Local Similarity   100.0%;  Pred. No. 0.016;
Matches    9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy         41 SALLRSIPA 49
              |||||||||
Db          2 SALLRSIPA 10


RESULT 7
US-07-871-973A-2
Sequence 2, Application US/07871973A
Patent No. 5767240
GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Gozes, Illana
; TITLE OF INVENTION: Activity-Dependent Neurotrophic Factor
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/871,973A
; FILING DATE: 22-APR-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,087
; FILING DATE: 22-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
```

;   REFERENCE/DOCKET NUMBER: 15280-178
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 14 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: one-of(2, 3, 4)
;   OTHER INFORMATION: /product= "Xaa = unsure amino acid"
US-07-871-973A-2

Qy   41 SALLRSIPA 49
        |||||||||
Db   5 SALLRSIPA 13

Query Match   33.3%; Score 40; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-08-324-297A-1
; Sequence 1, Application US/08324297A
; Patent No. 6174862
; GENERAL INFORMATION:
;   APPLICANT: Brenneman, Douglas E.
;   APPLICANT: Gozes, Illana
;   TITLE OF INVENTION: Neurotrophic Peptides of Activity
;   Dependent Neurotrophic Factor
;   NUMBER OF SEQUENCES: 21
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew
;   STREET: One Market Plaza, Steuart Street Tower
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105-1492
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/324,297A
;   FILING DATE: 17-OCT-1994
;   CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/871,973
;   FILING DATE: 22-APR-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/688,087
;   FILING DATE: 22-APR-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Garrett-Wackowski, Eugenia
;   REGISTRATION NUMBER: 37,330
;   REFERENCE/DOCKET NUMBER: 15280-178-1US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 543-9600
;   TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 14 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-324-297A-1

RESULT 9
US-09-187-330-23
; Sequence 23, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
;   APPLICANT: Gozes, Illana
;   APPLICANT: Brenneman, Douglas E.
;   APPLICANT: Bassan, Merav
;   APPLICANT: Zamostiano, Rachel
;   APPLICANT: The Government of the United States of America
;   as represented by the Secretary of the
;   APPLICANT: Department of Health and Human Services
;   TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
;   FILE REFERENCE: 015280-2912000US
;   CURRENT APPLICATION NUMBER: US/09/187,330
;   CURRENT FILING DATE: 1998-11-06
;   EARLIER APPLICATION NUMBER: US 60/037,404
;   EARLIER FILING DATE: 1997-02-07
;   EARLIER APPLICATION NUMBER: WO PCT/US98/02485
;   EARLIER FILING DATE: 1998-02-06
;   NUMBER OF SEQ ID NOS: 63
;   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:active peptide
;   OTHER INFORMATION: of ADNF I hsp60-related sequence
US-09-187-330-23

Qy   41 SALLRSIPA 49
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Db   6 SALLRSIPA 14

Query Match   33.3%; Score 40; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
US-09-187-330-21
; Sequence 21, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
;   APPLICANT: Gozes, Illana
;   APPLICANT: Brenneman, Douglas E.
;   APPLICANT: Bassan, Merav
;   APPLICANT: Zamostiano, Rachel
;   APPLICANT: The Government of the United States of America
;   as represented by the Secretary of the
;   APPLICANT: Department of Health and Human Services
;   TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
;   FILE REFERENCE: 015280-2912000US
;   CURRENT APPLICATION NUMBER: US/09/187,330
;   CURRENT FILING DATE: 1998-11-06
;   EARLIER APPLICATION NUMBER: US 60/037,404
;   EARLIER FILING DATE: 1997-02-07
;   EARLIER APPLICATION NUMBER: WO PCT/US98/02485
;   EARLIER FILING DATE: 1998-02-06
;   NUMBER OF SEQ ID NOS: 63
;   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21

LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF
OTHER INFORMATION: I/hsp60-related sequence conjugated through the
OTHER INFORMATION: Cys residue to Sephadex for affinity
OTHER INFORMATION: chromatography
US-09-187-330-21

```
Qy    41 SALLRSIPA 49
         |||||||||
Db     7 SALLRSIPA 15
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Query Match   33.3%; Score 40; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
US-08-324-297A-6
Sequence 6, Application US/0832429A
Patent No. 6174862
GENERAL INFORMATION:
APPLICANT: Brenneman, Douglas E.
APPLICANT: Gozes, Illana
TITLE OF INVENTION: Neurotrophic Peptides of Activity
TITLE OF INVENTION: Dependent Neurotrophic Factor
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,297A
FILING DATE: 17-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,973
FILING DATE: 22-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,087
FILING DATE: 22-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-178-1US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-324-297A-6

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Qy    41 SALLRSIPA 49
         |||||||||
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Query Match   33.3%; Score 40; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    41 SALLRSIPA 49
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Db    11 SALLRSIPA 19
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RESULT 12
US-08-379-613-5
Sequence 5, Application US/0837961
Patent No. 5736146
GENERAL INFORMATION:
APPLICANT: Cohen, Irun R.
APPLICANT: Fridkin, Matityahu
APPLICANT: Konen-Waisman, Stephanie
TITLE OF INVENTION: Conjugates of Poorly Immunogenic
TITLE OF INVENTION: Antigens and Synthetic Peptide Carriers and Vaccines
TITLE OF INVENTION: Comprising Them.
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,613
FILING DATE: 22-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7534-013-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-8864/9741
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..24
OTHER INFORMATION: /label= Pep277S
US-08-379-613-5

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Qy    41 SALLRSIPA 49
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Db     6 SALLRSIPA 14
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Query Match   33.3%; Score 40; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
US-08-324-297A-5
Sequence 5, Application US/08324297A
Patent No. 6174862
GENERAL INFORMATION:
APPLICANT: Brenneman, Douglas E.
APPLICANT: Gozes, Illana
TITLE OF INVENTION: Neurotrophic Peptides of Activity
TITLE OF INVENTION: Dependent Neurotrophic Factor
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,297A
FILING DATE: 17-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,973
FILING DATE: 22-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,087
FILING DATE: 22-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-178-1US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-324-297A-5

Query Match   30.0%; Score 36; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches   8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   42  ALLRSIPA  49
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Db    1  ALLRSIPA  8
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RESULT 14
US-08-324-297A-7
Sequence 7, Application US/08324297A
Patent No. 6174862
GENERAL INFORMATION:
APPLICANT: Brenneman, Douglas E.
APPLICANT: Gozes, Iliana
TITLE OF INVENTION: Neurotrophic Peptides of Activity
TITLE OF INVENTION: Dependent Neurotrophic Factor
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,297A
FILING DATE: 17-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,973
FILING DATE: 22-APR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,087
FILING DATE: 22-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-178-1US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-324-297A-7

Query Match   28.3%; Score 34; DB 3; Length 9;
Best Local Similarity   77.8%; Pred. No. 4.1e+05;
Matches   7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy   41  SALLRSIPA  49
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Db    1  TALLRTIPA  9
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RESULT 15
US-09-248-796A-19008
Sequence 19008, Application US/0924879 6A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19008
LENGTH: 409
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-19008

Query Match   27.5%; Score 33; DB 4; Length 409;
Best Local Similarity   77.8%; Pred. No. 32;
Matches   7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy   41  SALLRSIPA  49
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Db  212  SALLQAIPA  220
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Search completed: February 23, 2005, 19:36:08
Job time : 31.1695 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: February 23, 2005, 19:34:28 ; Search time 89 Seconds
(without alignments)
327.241 Million cell updates/sec

Title: US-09-267-511-3
Perfect score: 120
Sequence: 1 XXXXXXXXXXXXXXXXXXXXX..........XXXXXXXXXXXXXXXXXXXX 89

Scoring table: BLOSUM62
Scoring: Gapop 10.0, Gapext 0.5

Searched: 1380268 seqs, 327241040 residues
Total number of hits satisfying chosen parameters: 1380268

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database : Published_Applications_AA:*
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3: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	40	33.3	9	9	US-09-267-511-1	Sequence 1, Appli
2	40	33.3	9	14	US-10-164-432-3	Sequence 3, Appli
3	40	33.3	9	15	US-10-296-849-1	Sequence 1, Appli
4	40	33.3	9	15	US-10-623-272-5	Sequence 5, Appli
5	40	33.3	9	15	US-10-623-272-36	Sequence 36, Appli
6	40	33.3	10	14	US-10-164-432-5	Sequence 5, Appli
7	40	33.3	10	15	US-10-296-849-19	Sequence 19, Appl
8	40	33.3	10	15	US-10-623-272-22	Sequence 22, Appl
9	40	33.3	11	15	US-10-296-849-18	Sequence 18, Appl
10	40	33.3	12	15	US-10-296-849-17	Sequence 17, Appl
11	40	33.3	13	15	US-10-296-849-16	Sequence 16, Appl
12	40	33.3	14	9	US-10-267-511-21	Sequence 21, Appl
13	40	33.3	14	14	US-10-164-432-6	Sequence 6, Appli
14	40	33.3	14	15	US-10-296-849-14	Sequence 14, Appl
15	40	33.3	14	15	US-10-623-272-23	Sequence 23, Appl
16	40	33.3	15	15	US-10-623-272-21	Sequence 21, Appl
17	40	33.3	18	15	US-10-164-432-8	Sequence 8, Appli
18	40	33.3	19	16	US-09-267-511-14	Sequence 14, Appl
19	40	33.3	19	16	US-09-267-511-16	Sequence 16, Appl
20	40	33.3	19	16	US-09-267-511-17	Sequence 17, Appl
21	40	33.3	19	14	US-09-267-511-22	Sequence 22, Appl
22	40	33.3	19	15	US-10-164-432-7	Sequence 7, Appl
23	40	33.3	19	15	US-10-164-432-8	Sequence 8, Appl
24	40	33.3	89	15	US-09-267-511-3	Sequence 3, Appli
25	40	33.3	89	15	US-09-267-511-3	Sequence 3, Appli
26	34	28.3	9	14	US-10-296-849-3	Sequence 3, Appli
27	34	28.3	126	15	US-10-437-963-153367	Sequence 135367,
28	34	28.3	148	16	US-10-437-963-168965	Sequence 168965,
29	34	28.3	882	16	US-10-437-963-145870	Sequence 145870,
30	34	28.3	1314	16	US-10-437-963-134696	Sequence 134696,
31	34	28.3	1414	16	US-10-437-963-118711	Sequence 118711,
32	33	27.5	1632	16	US-10-437-963-118708	Sequence 118708,
33	33	27.5	310	15	US-10-282-122A-69367	Sequence 69367, A
34	33	27.5	394	14	US-10-032-585-7381	Sequence 7381, Ap
35	32	26.7	288	15	US-10-425-114-70419	Sequence 70419, A
36	32	26.7	327	15	US-10-369-493-22368	Sequence 22368, A
37	32	26.7	390	16	US-10-767-701-45954	Sequence 45954, A
38	32	26.7	394	16	US-10-425-114-71002	Sequence 71002, A
39	32	26.7	459	16	US-10-437-963-160947	Sequence 160947,
40	32	26.7	473	16	US-09-815-242-11235	Sequence 11235,
41	32	26.7	473	9	US-10-282-122A-11235	Sequence 11235, A
42	32	26.7	516	15	US-10-282-122A-48070	Sequence 48070, A
43	32	26.7	787	16	US-10-282-122A-58506	Sequence 58506, A
44	32	26.7	1332	15	US-10-369-493-15830	Sequence 15830, A
45	32	26.7	1332	15	US-10-369-493-16211	Sequence 16211, A

ALIGNMENTS

RESULT 1
US-09-267-511-1
; Sequence 1, Application US/09267511
; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-37700US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:activity
; OTHER INFORMATION: dependent neurotrophic factor I (ADNF I) active
; OTHER INFORMATION: site
US-09-267-511-1

Query Match 33.3%; Score 40; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        41 SALLRSIPA 49
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Db         1 SALLRSIPA 9

RESULT 2
US-10-164-432-3
; Sequence 3, Application US/10164432
; Publication No. US20030165441A1
; GENERAL INFORMATION:
;  APPLICANT: Alcon Inc.
;  APPLICANT: Clark, Abbot F.
;  APPLICANT: Debra, Shade L.
;  TITLE OF INVENTION: The Use of ADNP for the Treatment of Glaucomatous Optic Neuropath
;  FILE REFERENCE: 1975A US
;  CURRENT APPLICATION NUMBER: US/10/164,432
;  CURRENT FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: 09/921,029
;  PRIOR APPLICATION FILING DATE: 2001-08-02
;  PRIOR APPLICATION NUMBER: 60/230,964
;  PRIOR FILING DATE: 2000-09-07
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: Patentin version 3.1
;  SEQ ID NO 3
;  LENGTH: 9
;  TYPE: PRT
;  ORGANISM: homo sapiens
US-10-164-432-3

Qy   Query Match       33.3%;  Score 40;  DB 14;  Length 9;
Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
Matches       9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        41 SALLRSIPA 49
             ||||||||||
Db         1 SALLRSIPA 9

RESULT 3
US-10-296-849-1
; Sequence 1, Application US/10296849
; Publication No. US20040048801A1
; GENERAL INFORMATION:
;  APPLICANT: Spong, Catherine Y.
;  APPLICANT: Brenneman, Douglas
;  APPLICANT: Gozes, Illana
;  APPLICANT: The Government of the United States of America
;  APPLICANT:   as represented by the Secretary of the
;  APPLICANT:   Department of Health and Human Services
;  APPLICANT: Ramot University Authority for Applied and
;  APPLICANT:   Industrial Development, Ltd.
;  TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
;  FILE REFERENCE: 15280W-004200US
;  CURRENT APPLICATION NUMBER: US/10/296,849
;  CURRENT FILING DATE: 2003-06-18
;  PRIOR APPLICATION NUMBER: US 60/208,944
;  PRIOR FILING DATE: 2000-05-31
;  PRIOR APPLICATION NUMBER: US 60/267,805
;  PRIOR FILING DATE: 2001-02-08
;  PRIOR APPLICATION NUMBER: WO PCT/US01/17758
;  PRIOR FILING DATE: 2001-05-31
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 1
;  LENGTH: 9
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence:Activity
;  OTHER INFORMATION: Dependent Neurotrophic Factor I (ADNF I) active
;  OTHER INFORMATION: core site, SAL or ADNF-9
US-10-296-849-1
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Qy   Query Match       33.3%;  Score 40;  DB 15;  Length 9;
Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
Matches       9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        41 SALLRSIPA 49
             ||||||||||
Db         1 SALLRSIPA 9

RESULT 4
US-10-623-272-5
; Sequence 5, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
;  APPLICANT: Gozes, Illana
;  APPLICANT: Brenneman, Douglas E.
;  APPLICANT: Bassan, Merav
;  APPLICANT: Zamostiano, Rachel
;  APPLICANT: The Government of the United States of America
;  APPLICANT:   as represented by the Secretary of the
;  APPLICANT:   Department of Health and Human Services
;  TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
;  FILE REFERENCE: 015280-2912OOUS
;  CURRENT APPLICATION NUMBER: US/10/623,272
;  CURRENT FILING DATE: 2003-07-17
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
;  PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: Patentin Ver. 2.0
;  SEQ ID NO 5
;  LENGTH: 9
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence:ADNF-9 active
;  OTHER INFORMATION: peptide antigen
US-10-623-272-5

Qy   Query Match       33.3%;  Score 40;  DB 15;  Length 9;
Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
Matches       9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        41 SALLRSIPA 49
             ||||||||||
Db         1 SALLRSIPA 9

RESULT 5
US-10-623-272-36
; Sequence 36, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
;  APPLICANT: Gozes, Illana
;  APPLICANT: Brenneman, Douglas E.
;  APPLICANT: Bassan, Merav
;  APPLICANT: Zamostiano, Rachel
;  APPLICANT: The Government of the United States of America
;  APPLICANT:   as represented by the Secretary of the
;  APPLICANT:   Department of Health and Human Services
;  TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
;  FILE REFERENCE: 015280-2912OOUS
;  CURRENT APPLICATION NUMBER: US/10/623,272
;  CURRENT FILING DATE: 2003-07-17
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
;  PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
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; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.0
;
SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
; OTHER INFORMATION: peptide adsorbed onto bovine serum albumin (BSA)
; ORGANISM: as antigen
US-10-623-272-36

  Query Match       33.3%;  Score 40;  DB 15;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches   9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      41  SALLRSIPA  49
            |||||||||
Db       1  SALLRSIPA  9

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US-10-164-432-5
; Sequence 5, Application US/10164432
; Publication No. US20030166544A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Inc.
; APPLICANT: Clark, Abbot F.
; APPLICANT: Debra, Shade L.
; TITLE OF INVENTION: The Use of ADNF for the Treatment of Glaucomatous Optic Neuropath
; FILE REFERENCE: 1975A US
; CURRENT APPLICATION NUMBER: US/10/164,432
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/921,029
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/230,964
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-164-432-5

  Query Match       33.3%;  Score 40;  DB 14;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      41  SALLRSIPA  49
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Db       2  SALLRSIPA  10

RESULT 7
US-10-296-849-19
; Sequence 19, Application US/10296849
; Publication No. US20040048801A1
; GENERAL INFORMATION:
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Brenneman, Douglas
; APPLICANT: Gozes, Illana
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied and
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
; FILE REFERENCE: 15280W-0042OOUS
; CURRENT APPLICATION NUMBER: US/10/296,849
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/208,944
; PRIOR FILING DATE: 2000-05-31
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; PRIOR APPLICATION NUMBER: US 60/267,805
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: WO PCT/US01/17758
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
;
SEQ ID NO 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF I
; OTHER INFORMATION: polypeptide
US-10-296-849-19

  Query Match       33.3%;  Score 40;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      41  SALLRSIPA  49
            |||||||||
Db       2  SALLRSIPA  10

RESULT 8
US-10-623-272-22
; Sequence 22, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-29120OUS
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.0
;
SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: conjugated through the Cys residue to Sephadex for
; OTHER INFORMATION: affinity chromatography
US-10-623-272-22

  Query Match       33.3%;  Score 40;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      41  SALLRSIPA  49
            |||||||||
Db       2  SALLRSIPA  10

RESULT 9
US-10-296-849-18
; Sequence 18, Application US/10296849
; Publication No. US20040048801A1
; GENERAL INFORMATION:
; APPLICANT: Spong, Catherine Y.
```

; APPLICANT: Brenneman, Douglas
; APPLICANT: Gozes, Illana
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied and
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
; FILE REFERENCE: 15280W-00420OUS
; CURRENT APPLICATION NUMBER: US/10/296,849
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/208,944
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 60/267,805
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: WO PCT/US01/17758
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF I
; OTHER INFORMATION: polypeptide
US-10-296-849-18

Query Match   33.3%;   Score 40;   DB 15;   Length 11;
Best Local Similarity   100.0%;   Pred. No. 0.19;
Matches   9;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   41   SALLRSIPA   49
             |||||||||
Db   3   SALLRSIPA   11

RESULT 10
US-10-296-849-17
; Sequence 17, Application No. US20040048801A1
; Publication No. US20040048801A1
; GENERAL INFORMATION:
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Brenneman, Douglas
; APPLICANT: Gozes, Illana
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied and
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
; FILE REFERENCE: 15280W-00420OUS
; CURRENT APPLICATION NUMBER: US/10/296,849
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/208,944
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 60/267,805
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: WO PCT/US01/17758
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF I
; OTHER INFORMATION: polypeptide
US-10-296-849-17

Query Match   33.3%;   Score 40;   DB 15;   Length 12;
Best Local Similarity   100.0%;   Pred. No. 0.21;

Matches   9;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   41   SALLRSIPA   49
             |||||||||
Db   4   SALLRSIPA   12

RESULT 11
US-10-296-849-16
; Sequence 16, Application US/10296849
; Publication No. US20040048801A1
; GENERAL INFORMATION:
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Brenneman, Douglas
; APPLICANT: Gozes, Illana
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied and
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
; FILE REFERENCE: 15280W-00420OUS
; CURRENT APPLICATION NUMBER: US/10/296,849
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/208,944
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 60/267,805
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: WO PCT/US01/17758
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF I
; OTHER INFORMATION: polypeptide
US-10-296-849-16

Query Match   33.3%;   Score 40;   DB 15;   Length 13;
Best Local Similarity   100.0%;   Pred. No. 0.23;
Matches   9;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   41   SALLRSIPA   49
             |||||||||
Db   5   SALLRSIPA   13

RESULT 12
US-09-267-511-21
; Sequence 21, Application US/09267511
; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-37700US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 21

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;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:ADNF I
;   OTHER INFORMATION: polypeptide
US-09-267-511-21

Query Match
Best Local Similarity  33.3%;  Score 40;  DB 9;  Length 14;
Matches  9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    41  SALLRSIPA  49
          |||||||||
Db     6  SALLRSIPA  14

RESULT 13
US-10-164-432-6
; Sequence 6, Application US/10164432
; Publication No. US20030166544A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Inc.
; APPLICANT: Clark, Abbot F.
; APPLICANT: Debra, Shade L.
; CURRENT FILING DATE: 2002-06-06
; FILE REFERENCE: 1975A US
; TITLE OF INVENTION: The Use of ADNF for the Treatment of Glaucomatous Optic Neuropath
; CURRENT APPLICATION NUMBER: 09/921,029
; PRIOR APPLICATION NUMBER: US/10/164,432
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/230,964
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 6
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-164-432-6
; SOFTWARE: Patentin version 3.1

Query Match
Best Local Similarity  33.3%;  Score 40;  DB 14;  Length 14;
Matches  9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    41  SALLRSIPA  49
          |||||||||
Db     6  SALLRSIPA  14

RESULT 14
US-10-296-849-14
; Sequence 14, Application US/10296849
; Publication No. US20040048801A1
; GENERAL INFORMATION:
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Brenneman, Douglas
; APPLICANT: Gozes, Iliana
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied and
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
; FILE REFERENCE: 15280W-0042000US
; CURRENT APPLICATION NUMBER: US/10/296,849
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/208,944
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 60/267,805
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: WO PCT/US01/17758
; PRIOR FILING DATE: 2001-05-31

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:ADNF I
;   OTHER INFORMATION: polypeptide
US-10-296-849-14

Query Match
Best Local Similarity  33.3%;  Score 40;  DB 15;  Length 14;
Matches  9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    41  SALLRSIPA  49
          |||||||||
Db     6  SALLRSIPA  14

RESULT 15
US-10-623-272-23
; Sequence 23, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Iliana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-2912000US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:active peptide
;   OTHER INFORMATION: of ADNF I hsp60-related sequence
US-10-623-272-23

Query Match
Best Local Similarity  33.3%;  Score 40;  DB 15;  Length 14;
Matches  9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    41  SALLRSIPA  49
          |||||||||
Db     6  SALLRSIPA  14

Search completed: February 23, 2005, 19:51:27
Job time : 90 secs
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: February 23, 2005, 19:22:32 ; Search time 24.6384 Seconds
                 (without alignments)
                 347.559 Million cell updates/sec

Title: US-09-267-511-3
Perfect score: 120
Sequence: 1 XXXXXXXXXXXXXXXXXXXXX...........XXXXXXXXXXXXXXXX 89

Scoring table: BLOSUM62
                 Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_79:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	35	29.2	286	2	T05061	hypothetical prote
2	34	28.3	642	2	AE2407	serine/threonine k
3	33	27.5	430	2	C86825	uracil permease [i
4	33	27.5	3530	2	A59266	unconventional myo
5	32	26.7	181	2	D86518	hypothetical prote
6	32	26.7	181	2	C72104	hypothetical prote
7	32	26.7	225	2	H82148	amino acid ABC tra
8	32	26.7	327	2	S61660	probable membrane
9	32	26.7	330	2	F72331	conserved hypothet
10	32	26.7	331	2	C72424	oligopeptide ABC t
11	32	26.7	440	2	A84387	oligopeptide ABC t
12	32	26.7	473	2	E64120	exodeoxyribonuclea
13	32	26.7	569	2	S11035	chaperonin hsp60,
14	31	25.8	216	2	E70037	serine O-acetyltra
15	31	25.8	247	2	C84798	hypothetical prote
16	31	25.8	250	2	T23185	hypothetical prote
17	31	25.8	286	2	T38768	probable sec14 cyt
18	31	25.8	301	2	A82601	aspartyl/asparagin
19	31	25.8	332	2	C72300	oligopeptide ABC t
20	31	25.8	344	2	C97381	glucokinase (gluco
21	31	25.8	344	2	AB2599	glucokinase [impor
22	31	25.8	367	2	S59146	ubiquinol-cytochro
23	31	25.8	559	1	WMBBS1	71K upper matrix p
24	31	25.8	573	2	A32800	chaperonin GroEL p
25	31	25.8	573	1	HHMS60	chaperonin groEL p
26	31	25.8	573	2	HHRT60	chaperonin groEL p
27	31	25.8	573	2	A34173	chaperonin groEL p
28	31	25.8	671	2	T36037	probable export as
29	31	25.8	933	2	H69045	hypothetical prote
30	31	25.8	2413	2	S34670	splicing factor PR
31	31	25.8	2475	2	S35307	polyprotein pp220
32	31	25.0	144	2	B87693	conserved hypothet
33	30	25.0	206	2	A56617	cfaA protein precu
34	30	25.0	269	2	C71255	conserved hypothet
35	30	25.0	297	2	S35974	pecM protein - Erw
36	30	25.0	299	2	B83081	hypothetical prote
37	30	25.0	308	1	S22931	ubiquinol-cytochro
38	30	25.0	308	2	S22921	ubiquinol-cytochro
39	30	25.0	308	2	S22925	ubiquinol-cytochro
40	30	25.0	308	2	S22929	ubiquinol-cytochro
41	30	25.0	308	2	S22919	ubiquinol-cytochro
42	30	25.0	308	2	S22924	ubiquinol-cytochro
43	30	25.0	308	2	S22927	ubiquinol-cytochro
44	30	25.0	308	2	S22930	ubiquinol-cytochro
45	30	25.0	308	2	S22920	ubiquinol-cytochro

ALIGNMENTS

RESULT 1
T05061
hypothetical protein M3E9.140 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05061
R;Bevan, M.; Vandenbol, M.; Jallet, C.; Portetelle, D.; Hoheisel, J.; Mewes, H.W.; Maye
R;Bevan, M.
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15396
A;Molecule type: DNA
A;Residues: 1-286 <BEV>
A;Cross-references: UNIPROT:O65591; EMBL:AL022223
A;Experimental source: cultivar Columbia; BAC clone M3E9
C;Genetics:
A;Map position: 4
A;Introns: 100/1; 129/3; 161/1; 181/3; 208/1; 241/3; 260/2
A;Note: M3E9.140

Query Match		29.2%; Score 35; DB 2; Length 286;
Best Local Similarity		77.8%; Pred. No. 6.7;
Matches	7;	Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy   41 SALLRSIPA 49
            |:||||:|:|
Db   221 SSLLRSLPA 229

RESULT 2
AE2407
serine/threonine kinase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2407
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A;Reference number: AE1807; MUID:21595285; PMID:11759840
A;Accession: AE2407
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-642 <KUR>
A;Cross-references: UNIPROT:Q8YMW1; GB:BA000019; PIDN:BAB76512.1; PID:g17133950; GSPDB:
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: pknC

Query Match		28.3%; Score 34; DB 2; Length 642;
Best Local Similarity		87.5%; Pred. No. 26;
Matches	7;	Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   42 ALLRSIPA 49
          |:||||||||
Db   519 AMLRSIPA 526

RESULT 3
C86825
uracil permease [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86825
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86825
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-430 <STO>
A;Cross-references: UNIPROT:Q9CF78; GB:AE005176; PID:g12724609; PIDN:AAK05701.1; GSPDB:G
A;Experimental source: strain IL1403
A;Genetics:
A;Gene: pyrP
C;Superfamily: uracil transport protein uraA

Qy   41 SALLRSIPA 49
          |:||||:|||
Db   339 TALLQSIPA 347

Query Match   27.5%;   Score 33; DB 2; Length 430;
Best Local Similarity   77.8%;   Pred. No. 28;
Matches   7;   Conservative   2;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 4
A59266
unconventional myosin-15 - human
C;Species: Homo sapiens (man)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: A59266
R;Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Mi
an, T.B.; Friedell, R.A.
Genomics 61, 243-258, 1999
A;Title: Characterization of the human and mouse unconventional myosin XV genes responsi
A;Reference number: A59266; MUID:20021762; PMID:10552926
A;Accession: A59266
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-3530 <LIA>
A;Cross-references: UNIPROT:Q9UKN7; GB:AF144094; NID:g6224682; PIDN:AAF05903.1; PID:g622
F;1225-1887/Domain: myosin motor domain homology <MMO>

Qy   41 SALLRSIPA 49
          |:||||:|||
Matches   7;   Conservative   1;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   41 SALLRSIPA 49
          |||||:|||
Db   2482 SAALRSLPA 2490

RESULT 5
D86518
hypothetical protein CPj0220 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86518
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: D86518
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-181 <STO>
A;Cross-references: UNIPROT:Q9Z8W4; GB:BA000008; NID:g8978593; PIDN:BAA98430.1; GSPDB:GN
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0220

Qy   42 ALLRSIP 48
          |||||||
Db   52 ALLRSIP 58

RESULT 6
C72104
hypothetical protein CP0545 [imported] - Chlamydophila pneumoniae (strains CWL029 and A
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: C72104; B81567
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: C72104
A;Molecule type: DNA
A;Residues: 1-181 <ARN>
A;Cross-references: UNIPROT:Q9Z8W4; GB:AE001608; GB:AE001363; NID:g4376487; PIDN:AAD183
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: B81567
A;Molecule type: DNA
A;Residues: 1-181 <REA>
A;Cross-references: GB:AE002213; GB:AE002161; NID:g7189446; PIDN:AAF38367.1; PID:g71894
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CPn0220; CP0545

Query Match   26.7%;   Score 32; DB 2; Length 181;
Best Local Similarity   100.0%;   Pred. No. 19;
Matches   7;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   42 ALLRSIP 48
          |||||||
Db   52 ALLRSIP 58

RESULT 7
H82148
amino acid ABC transporter, permease protein VC1861 [imported] - Vibrio cholerae (strai
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: H82148
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: H82148
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-225 <HBI>
A;Cross-references: UNIPROT:Q9KQY6; GB:AE004261; GB:AE003852; NID:g9655382; PIDN:AAF950
A;Experimental source: aerogroup O1; strain N16961; biotype El Tor

Query Match   26.7%;   Score 32; DB 2; Length 181;
Best Local Similarity   100.0%;   Pred. No. 19;
Matches   7;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
RESULT 8
S61660
probable membrane protein YOR100c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O3193; hypothetical protein YOR3193c
C;Species: Saccharomyces cerevisiae
C;Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 19-Apr-2002
C;Accession: S61660; S66985
R;Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banrevi, A.; Sander, C.; Valencia,
C.M.
submitted to the EMBL Data Library, December 1995
A;Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome
submitted to the Protein Sequence Database, July 1996
A;Accession: S66985
A;Molecule type: DNA
A;Reference number: S61643
A;Accession: S61660
A;Molecule type: DNA
A;Residues: 1-327 <BEN>
A;Cross-references: EMBL:X94335; NID:g1262139; PID:g1164947
R;Voss, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansorge, W.
A;Accession: S66985
A;Molecule type: DNA
A;Residues: 1-327 <VOS>
A;Cross-references: EMBL:Z75008; NID:g1420278; PID:g1420279; MIPS:YOR100c
A;Experimental source: strain S288C
A;Genetics:
A;Gene: SGD:CRC1
A;Cross-references: SGD:S005626
A;Map position: 15R
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: transmembrane protein
F;32-127/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;101-117/Domain: transmembrane #status predicted <TM1>
F;138-222/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;236-322/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;242-258/Domain: transmembrane #status predicted <TM2>

Qy          41 SALLRSIPA 49
               ||| ||:||
Db         143 SALLRSLPA 151


RESULT 9
F72331
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: F72331
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72331
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-330 <ARN>

Qy          42 ALLRSIPA 49
               |||||:||
Db         300 ALLRSPPA 307
```



```
A;Cross-references: UNIPROT:Q9WZS0; GB:AE001748; GB:AE000512; NID:g4981332; PID:AAD358
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0813

Qy          41 SALLRSIPA 49
               ||  ||:: ||
Db         295 SAPLRTVPA 303


RESULT 10
C72424
oligopeptide ABC transporter, ATP-binding protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: C72424
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-331 <ARN>
A;Cross-references: UNIPROT:Q9WXR4; GB:AE001692; GB:AE000512; NID:g4980535; PIDN:AAD351
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0058
C;Superfamily: inner membrane protein malk; ATP-binding cassette homology <ABC>
F;24-237/Domain: ATP-binding cassette homology <ABC>

Qy          42 ALLRSIP 48
               |||||||
Db         259 ALLRSIP 265


RESULT 11
A84387
oligopeptide ABC transporter ATP-binding [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: A84387
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: A84387
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-440 <STO>
A;Cross-references: UNIPROT:Q9HMM0; GB:AE004437; NID:g10581771; PIDN:AAG20461.1; GSPDB:
A;Genetics:
A;Gene: appF

Qy          42 ALLRSIP 48
               |||||||
```

RESULT 12
E64120
exodeoxyribonuclease I (EC 3.1.11.1) - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
A;Accession: E64120
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.;
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.,
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: E64120
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-473 <TIGR>
A;Cross-references: UNIPROT:P45188; GB:U32818; GB:L42023; NID:g1574209; PIDN:AAC23023.1;
C;Superfamily: exodeoxyribonuclease I
C;Keywords: DNA repair; hydrolase

Qy   42 AILRSIPA 49
               |||:||||||
Db   379 AILRSLPA 386

Query Match   26.7%; Score 32; DB 2; Length 473;
Best Local Similarity   75.0%; Pred. No. 51;
Matches   6; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

RESULT 13
S11035
chaperonin hsp60, testis - tobacco budworm
C;Species: Heliothis virescens (tobacco budworm)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S11035
R;Miller, S.G.; Leclerc, R.F.; Erdos, G.W.
J. Mol. Biol. 214, 407-422, 1990
A;Title: Identification and characterization of a testis-specific isoform of a chaperoni
A;Reference number: S11035; MUID:90339485; PMID:1974308
A;Accession: S11035
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-569 <JMO>
A;Cross-references: UNIPROT:P25420; GB:X56034; NID:g296831; PIDN:CAA39509.1; PID:g2968321
A;Note: the sequence from Fig. 8 is inconsistent with that from Fig. 6 in having 45-Glu
C;Superfamily: chaperonin groEL

Qy   41 SAILRSIPA 49
               |||||:|||
Db   444 AAILRCIPA 452

Query Match   26.7%; Score 32; DB 2; Length 569;
Best Local Similarity   77.8%; Pred. No. 62;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

RESULT 14
E70037
serine O-acetyltransferase homolog yvfD - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: E70037
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho,
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.,
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel;
Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel;
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero;
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, F
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: E70037
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-216 <KUN>
A;Cross-references: UNIPROT:P71063; GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15429
A;Experimental source: strain 168
A;Gene: yvfD

Qy   41 SAILRSIP 48
               |||:||||
Db   187 SAVIRSIP 194

Query Match   25.8%; Score 31; DB 2; Length 216;
Best Local Similarity   75.0%; Pred. No. 38;
Matches   6; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

RESULT 15
C84798
hypothetical protein At2g37880 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84798
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84798
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-247 <STO>
A;Cross-references: UNIPROT:Q7XJQ1; GB:AE002093; NID:g4895196; PIDN:AAD32783.1; GSPDB:G
A;Genetics:
A;Gene: At2g37880
A;Map position: 2

Qy   41 SAILRSIP 48
               |||:||||
Db   142 SCILRSVP 149

Query Match   25.8%; Score 31; DB 2; Length 247;
Best Local Similarity   75.0%; Pred. No. 44;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Search completed: February 23, 2005, 19:35:03
Job time : 27.6384 secs

Db   265 AILRSIP 271

Qy   41 AILRSIPA 49
                |||||:||
Db   386 AILRSLPA 386

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: February 23, 2005, 19:09:56 ; Search time 115.65 Seconds
                 (without alignments)
                 394.078 Million cell updates/sec

Title: US-09-267-511-3
Perfect score: 120
Sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXXX..........XXXXXXXXXXXXXXXXXXXXX 89

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_03:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40	33.3	36	2	Q9QUV0	Q9quv0 rattus sp.
2	36	30.0	167	2	Q8UWF4	Q8uwf4 salmo salar
3	35	29.2	223	2	Q8RXW5	Q8rxw5 arabidopsis
4	35	29.2	286	2	Q65591	Q65591 arabidopsis
5	35	29.2	317	2	Q8W205	Q8w205 arabidopsis
6	35	29.2	318	2	Q8W1P0	Q8w1p0 arabidopsis
7	34	28.3	157	2	Q8SFX2	Q8sfx2 cherax tenu
8	34	28.3	379	2	Q9GBG9	Q9gbg9 mustela alt
9	34	28.3	394	2	Q8A9X9	Q8a9x9 bacteroides
10	34	28.3	395	2	Q64UD6	Q64ud6 bacteroides
11	34	28.3	422	2	Q73MJ6	Q73mj6 treponema d
12	34	28.3	432	2	Q8XK98	Q8xk98 clostridium
13	34	28.3	444	2	Q7S970	Q7s970 neurospora
14	34	28.3	642	2	Q9L423	Q9l423 anabaena sp
15	34	28.3	642	2	Q8YMW1	Q8ymw1 anabaena sp
16	34	28.3	1094	2	Q75M81	Q75m81 oryza sativ
17	34	28.3	1196	2	Q8BYA0	Q8bya0 mus musculu
18	34	28.3	1414	2	Q7XVW4	Q7xvw4 oryza sativ
19	33	27.5	234	1	MAUM_METFL	maum_metfl methylobaci
20	33	27.5	301	2	Q8PDF6	Q8pdf6 xanthomonas
21	33	27.5	355	2	Q87XV7	Q87xv7 pseudomonas
22	33	27.5	364	2	Q75PQ3	Q75pq3 antheraea y
23	33	27.5	395	2	Q7MVE1	Q7mve1 porphyromon
24	33	27.5	401	2	Q9RBG0	Q9rbg0 alcaligenes
25	33	27.5	415	2	Q89RR2	Q89rr2 bradyrhizob
26	33	27.5	430	2	Q9L4N7	Q9l4n7 lactococcus
27	33	27.5	430	2	Q9CF78	Q9cf78 lactococcus
28	33	27.5	434	2	Q7XQF3	Q7xqf3 oryza sativ
29	33	27.5	585	2	Q8H333	Q8h333 oryza sativ
30	33	27.5	1008	2	Q7KS58	Q7ks58 drosophila
31	33	27.5	1541	2	Q9VCX1	Q9vcx1 drosophila
32	32	27.5	3530	1	MY15_HUMAN	Q9ukn7 homo sapien
33	32	26.7	112	2	Q7P8Y5	Q7p8y5 rickettsia
34	32	26.7	122	2	Q6UAW8	Q6uaw8 bacteriopha
35	32	26.7	181	2	Q28W4	Q28w4 chlamydia p
36	32	26.7	202	2	Q6UAW9	Q6uaw9 bacteriopha
37	32	26.7	225	2	Q9KQY6	Q9kqy6 vibrio chol
38	32	26.7	309	2	Q6KC47	Q6kc47 prunus pers
39	32	26.7	317	2	Q6FXM7	Q6fxm7 candida gla
40	32	26.7	327	1	CRC1_YEAST	Q75b41 saccharomyc
41	32	26.7	329	2	Q12289	Q12289 ashbya goss
42	32	26.7	330	2	Q75B41	Q9wzs0 thermotoga
43	32	26.7	331	2	Q9WZS0	Q9wzs0 thermotoga
44	32	26.7	352	2	Q9WXR4	Q9wxr4 streptomyce
45	32	26.7	352	2	Q92N75	Q92n75 streptomyce
	32	26.7	356	1	Q05603	COBT_SALTY salmonella

ALIGNMENTS

RESULT 1
Q9QUV0

ID   Q9QUV0   PRELIMINARY;   PRT;   36 AA.
AC   Q9QUV0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Activity-dependent neurotrophic factor, ADNF=14 kDa NEUROPROTECTIVE
DE   peptide/heat shock protein 60 homolog (Fragment).
OS   Rattus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10118;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96217593; PubMed=8636410;
RA   Brenneman D.E., Gozes I.;
RT   "A femtomolar-acting neuroprotective peptide.";
RL   J. Clin. Invest. 97:2299-2307(1996).
KW   ATP-binding; Chaperone.
DR   Pfam; PF00118; Cpn60_TCP1; 1.
DR   InterPro; IPR002423; Cpn60_TCP1-1.
DR   InterPro; IPR008950; GroEL-ATPase.
DR   GO; GO:0006457; P:protein folding; IEA.
DR   GO; GO:0051082; F:unfolded protein binding; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
FT   NON_TER   1   1
FT   NON_TER   36   36
SQ   SEQUENCE   36 AA; 3757 MW; 59DF1043761AA5BD CRC64;

Query Match   33.3%; Score 40; DB 2; Length 36;
Best Local Similarity   100.0%; Pred. No. 0.42;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 SALLRSIPA 49
              |||||||||
Db   6 SALLRSIPA 14

RESULT 2
Q8UWF4

ID   Q8UWF4   PRELIMINARY;   PRT;   167 AA.
AC   Q8UWF4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Heat shock protein 60 (Fragment).
GN   Name=hsp60;
OS   Salmo salar (Atlantic salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX   NCBI_TaxID=8030;
RN   [1]

```
RP   SEQUENCE FROM N.A.
RA   Yaderie F., Male R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
DR   EMBL; AY049960; AAL29931.1; -.
OC   Spermatophyta; Magnoliophyta;
OC   Name=At4g26430;
GN   Name=At4g26430;
DE   Hypothetical protein At4g26430 (Fragment).
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0051082; F:unfolded protein binding; IEA.
DR   GO; GO:0006457; P:protein folding; IEA.
DR   GO; GO:0006986; P:response to unfolded protein; IEA.
DR   Pfam; PF00118; Cpn60_TCP1; 1.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   ATP-binding; Chaperone; Heat shock.
FT   NON_TER       1      1
FT   NON_TER     167    167
SQ   SEQUENCE   167 AA;  17350 MW;  2D6D4A1D962C7634 CRC64;

Qy   42 ALLRSIPA 49
         ||||||||
Db   53 ALLRSIPA 60

Query Match             30.0%;  Score 36;  DB 2;  Length 167;
Best Local Similarity   100.0%;          Pred. No. 16;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 3
ID   Q8RXW5      PRELIMINARY;      PRT;   223 AA.
AC   Q8RXW5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein At4g26430 (Fragment).
GN   Name=At4g26430;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA   Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA   Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA   Kamiya A., Karlin-Neumann G., Kawai J., Kim C.J., Lam B.J., Lin J.,
RA   Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA   Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA   Theologis A.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY080638; AAL85984.1; -.
DR   InterPro; IPR000555; Mov34_MPN_PAD1.
DR   Pfam; PF01398; Mov34; 1.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   223 AA;  25181 MW;  64892BBBE60166D7B CRC64;

Qy   41 SALLRSIPA 49
         |:|||||:||
Db  158 SSLLRSIPA 166

Query Match             29.2%;  Score 35;  DB 2;  Length 223;
Best Local Similarity   77.8%;          Pred. No. 36;
Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 4
ID   O65591      PRELIMINARY;      PRT;   286 AA.
AC   O65591;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein M3E9.140 (Hypothetical protein At4g26430).
GN   Name=M3E9.140; Synonyms=At4g26430;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bevan M., Vandenbol M., Jallet C., Portetelle D., Hoheisel J.,
RA   Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Vandenbol M., Jallet C., Portetelle D., Mewes H.W., Lemcke K.,
RA   Mayer K.F.X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL022223; CAA18227.1; -.
DR   EMBL; AL161565; CAB79498.1; -.
DR   PIR; T05061; T05061.
DR   InterPro; IPR003639; Mov34-1.
DR   InterPro; IPR000555; Mov34_MPN_PAD1.
DR   Pfam; PF01398; Mov34; 1.
DR   ProDom; PD363422; Mov34-1; 1.
DR   SMART; SM00232; JAB_MPN; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   286 AA;  31954 MW;  51008C281F029684 CRC64;

Qy   41 SALLRSIPA 49
         |:|||||:||
Db  221 SSLLRSIPA 229

Query Match             29.2%;  Score 35;  DB 2;  Length 286;
Best Local Similarity   77.8%;          Pred. No. 46;
Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 5
ID   Q8W205      PRELIMINARY;      PRT;   317 AA.
AC   Q8W205;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 20, Last annotation update)
DE   CSN complex subunit 6B (Transcription factor-like) (Hypothetical
DE   protein At4g26430).
GN   Name=CSN6B; Synonyms=At4g26430;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21607801; PubMed=11742986; DOI=10.1093/emboj/20.24.7096;
RA   Fu H., Reis N., Lee Y., Glickman M.H., Vierstra R.;
RT   "Subunit interaction maps for the regulatory particle of the 26S
RT   proteasome and the COP9 signalosome.";
RL   EMBO J. 20:7096-7107(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22088475; PubMed=12093376;
RA   Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA   Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT   "Full-length messenger RNA sequences greatly improve genome
```

RT   annotation.";
RL   Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA   Feldmann K.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA   Onodera C.S., Quach H.L., Tang C.C., Toriumi M., Wong C., Wu H.C.,
RA   Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
RA   Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
RA   Ecker J.R., Theologis A.;
RT   "Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases."
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;

Qy   41 SALLRSIPA 49
           |:||||:||:||
Db   252 SSLLRSLPA 260

Query Match   29.2%;   Score 35; DB 2; Length 317;
Best Local Similarity 77.8%;   Pred. No. 52; Mismatches 2;
Matches   7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
ID   Q8W1P0   PRELIMINARY;   PRT;   318 AA.
AC   Q8W1P0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   COP9 signalosome subunit 6.
GN   Name=CSN6B;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21558789; PubMed=11701877;
RA   Peng Z., Serino G., Deng X.W.;
RT   "Molecular characterization of subunit 6 of the COP9 signalosome and
RT   its role in multifaceted developmental processes in Arabidopsis.";
RL   Plant Cell 13:2393-2407(2001).
DR   EMBL; AF434762; AAL49561.1; -.
DR   Pfam; PF01398; Mov34; 1.
DR   ProDom; PD363422; Mov34-1; 1.
DR   SMART; SM00232; JAB_MPN; 1.
SQ   SEQUENCE 318 AA; 35493 MW; 6A06F21C8AEFA29 CRC64;

Qy   41 SALLRSIPA 49
           |:||||:||:||
Db   253 SSLLRSLPA 261

Query Match   29.2%;   Score 35; DB 2; Length 318;
Best Local Similarity 77.8%;   Pred. No. 52; Mismatches 2;
Matches   7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
ID   Q8SFX2
AC   Q8SFX2;

DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cytochrome b (Fragment).
GN   Name=Cytb;
OS   Cherax tenuimanus (Australian crayfish).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC   Parastacoidea; Parastacidae; Cherax.
OX   NCBI_TaxID=99755;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Munasinghe D.H.N., Murphy N.P., Austin C.M.;
RT   "Utility of mitochondrial DNA sequences from four gene regions for
RT   systematic studies of Australian freshwater crayfish of the genus
RT   Cherax (Decapoda: Parastacidae).";
RL   J. Crust. Biol. 23:402-417(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Munasinghe H.N., Austin C.M., Whisson G.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RA   Munasinghe H.N., Murphy N.P., Austin C.M.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC   complex (complex III or cytochrome b-c1 complex), which is a
CC   respiratory chain that generates an electrochemical potential
CC   coupled to ATP synthesis (By similarity)
CC   -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
CC   b562) is low-potential and absorbs at about 562 nm, and heme 2 (or
CC   BH or b566) is high-potential and absorbs at about 566 nm (By
CC   similarity).
CC   -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC   cytochrome c1 and the Rieske protein (By similarity).
CC   -!- SIMILARITY: Belongs to the cytochrome b family.
DR   EMBL; AF492797; AAM13682.1; -.
DR   EMBL; AF510177; AAM44277.1; -.
DR   EMBL; AF510179; AAM44279.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR005798; Cytb_b6_C.
DR   InterPro; IPR005797; Cytb_b6_N.
DR   Pfam; PF00032; Cytochrom_B_C; 1.
DR   Pfam; PF00033; Cytochrom_B_N; 1.
DR   PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
KW   Electron transport; Heme; Mitochondrion; Respiratory chain;
KW   Transmembrane; Transport.
FT   NON_TER   1   1
FT   NON_TER   157   157
SQ   SEQUENCE 157 AA; 17653 MW; 8E7A8A8BDB70FE70 CRC64;

Qy   41 SALLRSIP 48
           |:|||||||
Db   145 SAILRSIP 152

Query Match   28.3%;   Score 34; DB 2; Length 157;
Best Local Similarity 87.5%;   Pred. No. 40; Mismatches 1;
Matches   7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
ID   Q9GBG9
AC   Q9GBG9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

```
DE   Cytochrome b.
GN   Name=cytb;
OS   Mustela altaica (mountain weasel).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC   Mustela.
OX   NCBI_TaxID=92062;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21138802; PubMed=11245219;
RA   Hosoda T., Suzuki H., Harada M., Tsuchiya K., Han S.H., Zhang Y.,
RA   Kryukov A.P., Lin L.K.;
RT   "Evolutionary trends of the mitochondrial lineage differentiation in
RT   species of genera Martes and Mustela.";
RL   Genes Genet. Syst. 75:259-267(2000).
-!-  FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC       complex (complex III or cytochrome b-c1 complex), which is a
CC       respiratory chain that generates an electrochemical potential
CC       coupled to ATP synthesis (By similarity).
-!-  COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
CC       b562) is low-potential and absorbs at about 562 nm, and heme 2 (or
CC       BH or b566) is high-potential and absorbs at about 566 nm (By
CC       similarity).
-!-  SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC       cytochrome c1 and the Rieske protein (By similarity).
-!-  SIMILARITY: Belongs to the cytochrome b family.
     HSSP; P00157; 1BE3.
     EMBL; AB051239; BAB18191.1; -.
     GO; GO:0016021; C:integral to membrane; IEA.
     GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
     GO; GO:0005739; C:mitochondrion; IEA.
     GO; GO:0016491; F:oxidoreductase activity; IEA.
     GO; GO:0006118; P:electron transport; IEA.
     GO; GO:0006810; P:transport; IEA.
     InterPro; IPR005798; Cytb_b6_C.
     InterPro; IPR005797; Cytb_b6_N.
     Pfam; PF00032; Cytochrom_B_C; 1.
     Pfam; PF00033; Cytochrom_B_N; 1.
     PROSITE; PS00190; CYTOCHROME_B_HEME; 1.
     PROSITE; PS00192; CYTOCHROME_B_QO; UNKNOWN_1.
     PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
KW   Electron transport; Heme; Mitochondrion; Respiratory chain;
KW   Transmembrane; Transport.
SQ   SEQUENCE   379 AA;   42590 MW;   435AF969C9989960B CRC64;

Query Match             28.3%;  Score 34;  DB 2;  Length 379;
Best Local Similarity   87.5%;
Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
                                                Pred. No. 1e+02;

Qy    42 AILRSIPA 49
         ||||||||
Db   279 AILRSIPA 286
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RESULT 9
ID   Q8A9X9
AC   Q8A9X9;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative uracil permease (Uracil transporter).
GN   OrderedLocusNames=BT0686;
OS   Bacteroides thetaiotaomicron.
OC   Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC   Bacteroidaceae; Bacteroides.
OX   NCBI_TaxID=818;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VPI-5482 / ATCC 29148;
RX   MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA   Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA   Chiang H.C., Hooper L.V., Gordon J.I.;
RT   "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL   Science 299:2074-2076(2003).
     EMBL; AE016928; AAO75793.1; -.
     GO; GO:0016020; C:membrane; IEA.
     GO; GO:0005215; F:transporter activity; IEA.
     GO; GO:0006810; P:transport; IEA.
     InterPro; IPR006043; Xant/urac/vitC.
     InterPro; IPR006042; Xan_ur_permease.
     Pfam; PF00860; Xan_ur_permease; 1.
     TIGRFAMs; TIGR00801; ncs2; 1.
     PROSITE; PS01116; XANTH_URACIL_PERMASE; 1.
KW   Complete proteome.
SQ   SEQUENCE   394 AA;   41238 MW;   AF6D8B8E79D84FC9 CRC64;

Query Match             28.3%;  Score 34;  DB 2;  Length 394;
Best Local Similarity   77.8%;
Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
                                                Pred. No. 1e+02;

Qy    41 SALLRSIPA 49
         |||||:|||:
Db   307 SALLKSIPA 315
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RESULT 10
ID   Q64UD6
AC   Q64UD6;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative uracil permease.
GN   ORFNames=BF2146;
OS   Bacteroides fragilis.
OC   Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC   Bacteroidaceae; Bacteroides.
OX   NCBI_TaxID=817;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=YCH46;
RA   Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA   Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT   "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT   inversions regulating cell surface adaptation.";
RL   Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
     EMBL; AP006841; BAD48893.1; -.
SQ   SEQUENCE   395 AA;   41513 MW;   72C69337D0D258650 CRC64;

Query Match             28.3%;  Score 34;  DB 2;  Length 395;
Best Local Similarity   77.8%;
Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
                                                Pred. No. 1.1e+02;

Qy    41 SALLRSIPA 49
         |||||:|||:
Db   307 SALLKSIPA 315
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RESULT 11
ID   Q73MJ6
AC   Q73MJ6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Membrane protein, putative.
GN   OrderedLocusNames=TDE1512;
OS   Treponema denticola.
OC   Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX   NCBI_TaxID=158;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 35405 / DSM 14222;
RX   PubMed=15643399; DOI=10.1073/pnas.0307639101;
RA   Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
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RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
RA Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
DR EMBL; AE017251; AAS12029.1; -.
DR TIGR; TDE1512; -.
KW Complete proteome.
SQ SEQUENCE 422 AA; 48017 MW; 525219A73FD85E8E CRC64;

Qy   41 SALLRSIP 48
                ||:|:||||
Db   58 SALIRSIP 65

Query Match   28.3%; Score 34; DB 2; Length 422;
Best Local Similarity   87.5%; Pred. No. 1.2e+02;
Matches   7; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

RESULT 12
ID   Q8XK98   PRELIMINARY;   PRT;   432 AA.
AC   Q8XK98;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Probable uracil permease.
GN   Name=uraA; OrderedLocusNames=CPE1505;
OS   Clostridium perfringens.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1502;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=13;
RX   MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RA   Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA   Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT   "Complete genome sequence of Clostridium perfringens, an anaerobic
RT   flesh-eater.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR   EMBL; AP003190; BAB81211.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   Pfam; PF00860; Xan_ur_permease; 1.
DR   TIGRFAMs; TIGR00801; ncs2; 1.
DR   PROSITE; PS01116; XANTH_URACIL_PERMEASE; 1.
KW   Complete proteome.
SQ   SEQUENCE 432 AA; 45695 MW; 2E732D28AAE155A2 CRC64;

Qy   41 SALLRSIP 48
                ||||:||||
Db   337 SALIRSIP 344

Query Match   28.3%; Score 34; DB 2; Length 432;
Best Local Similarity   87.5%; Pred. No. 1.2e+02;
Matches   7; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

RESULT 13
ID   Q7S970   PRELIMINARY;   PRT;   444 AA.
AC   Q7S970;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.

GN   Name=NCU07298.1;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OR74A;
RX   MEDLINE=; PubMed=12712292;
RA   Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA   Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA   Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA   Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA   Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA   Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA   Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA   Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA   Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA   Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA   DeSouza C.C., Glass L., Orbach M.J., Berglund J.A., Voelker R.,
RA   Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA   Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA   Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT   "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL   Nature 0:0-0(2003).
CC   -!- CAUTION: The sequence shown here is derived from an
CC   EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC   preliminary data.
DR   EMBL; AABX01000217; EAA32916.1; -.
DR   HSSP; P77407; 1PQY.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR003673; CAIB_BAIF.
DR   Pfam; PF02515; CoA_transf_3; 1.
KW   Hypothetical protein.
SQ   SEQUENCE 444 AA; 48688 MW; 07C93D8D6B3106FD CRC64;

Qy   41 SALLRSIPA 49
                ||| ||||||
Db   13 SALLRSIPA 21

Query Match   28.3%; Score 34; DB 2; Length 444;
Best Local Similarity   88.9%; Pred. No. 1.2e+02;
Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 14
ID   Q9L423   PRELIMINARY;   PRT;   642 AA.
AC   Q9L423;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Serine/threonine kinase.
GN   Name=pknC;
OS   Anabaena sp. (strain PCC 7120).
OC   Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX   NCBI_TaxID=103690;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PCC 7120;
RA   Gonzalez L., Phalip V., Zhang C.C.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ251821; CAB75357.1; -.
DR   PhosSite; Q9L423; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004672; F:protein kinase activity; IEA.
DR   GO; GO:0004674; F:protein amino acid phosphorylation; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW   Kinase.
SQ   SEQUENCE 642 AA; 70785 MW; 81B3652C869E6B7 CRC64;

```
Query Match
Best Local Similarity      28.3%;      Score 34;  DB 2;  Length 642;
Matches      7;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

Qy        42 ALLRSIPA 49
             |:||||||
Db        519 AMLRSIPA 526


RESULT 15
Q8YMW1
ID   Q8YMW1;      PRELIMINARY;      PRT;      642 AA.
AC   Q8YMW1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Serine/threonine kinase.
GN   Name=pknC; OrderedLocusNames=all4813;
OS   Anabaena sp. (strain PCC 7120).
OC   Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX   NCBI_TaxID=103690;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21595285; PubMed=11759840;
RA   Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA   Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA   Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA   Yasuda M., Tabata S.;
RT   "Complete genomic sequence of the filamentous nitrogen-fixing
RT   cyanobacterium Anabaena sp. strain PCC 7120.";
RL   DNA Res. 8:205-213(2001).
DR   EMBL; AP003597; BAB76512.1; -.
DR   PIR; AE2407; AE2407.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004672; F:protein kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Complete proteome; Kinase.
SQ   SEQUENCE      642 AA;  70834 MW;  DBA9C8F3D27847AA CRC64;


Query Match
Best Local Similarity      28.3%;      Score 34;  DB 2;  Length 642;
Matches      7;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

Qy        42 ALLRSIPA 49
             |:||||||
Db        519 AMLRSIPA 526


Search completed: February 23, 2005, 19:34:16
Job time : 125.65 secs
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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: February 23, 2005, 19:09:01 ; Search time 118.825 Seconds
                                            (without alignments)
                                            286.429 Million cell updates/sec

Title: US-09-267-511-4
Perfect score: 121
Sequence: 1 XXXXXXXXXXXXXXXXXXXXXX..........XXXXXXXXXXXXXXXXXXXXX 88

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Maximum DB seq length: 2000000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
               1: geneseqp1990s:*
               2: geneseqp1990s:*
               3: geneseqp2000s:*
               4: geneseqp2001s:*
               5: geneseqp2002s:*
               6: geneseqp2003aa:*
               7: geneseqp2003ba:*
               8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	33.9	8	1	AAW64677	Aaw64677 Human ADN
2	41	33.9	8	2	AAW64678	Aaw64678 Human ADN
3	41	33.9	8	3	AAY71143	Aay71143 Human ADN
4	41	33.9	8	3	AAB23470	Aab23470 Activity
5	41	33.9	8	4	AAB23472	Aab23472 Activity
6	41	33.9	8	4	AAB72322	Aab72322 Activity
7	41	33.9	8	6	ABB07216	Abb07216 ADNF III
8	41	33.9	8	7	ABR39742	Abr39742 ADNF I ac
9	41	33.9	8	8	ADA07953	Ada07953 Human act
10	41	33.9	8	8	ADQ76121	Adq76121 ADNF III
11	41	33.9	8	2	ADS73609	Ads73609 ADNF III
12	41	33.9	10	2	AAW64696	Aaw64696 Seq ID 33
13	41	33.9	10	3	AAY71139	Aay71139 Human Act
14	41	33.9	10	3	AAB23488	Aab23488 Activity
15	41	33.9	10	4	AAB72323	Aab72323 Activity
16	41	33.9	10	5	AAB72328	Aab72328 Activity
17	41	33.9	10	5	ABB07223	Abb07223 ADNF III
18	41	33.9	10	8	ADQ76135	Adq76135 ADNF III
19	41	33.9	10	8	ADQ76131	Adq76131 ADNF III
20	41	33.9	10	8	ADQ76137	Adq76137 ADNF III
21	41	33.9	10	8	ADS73616	Ads73616 ADNF III
22	41	33.9	10	8	ADS73620	Ads73620 ADNF III
23	41	33.9	13	2	AAW64697	Aaw64697 Seq ID 34
24	41	33.9	13	2	AAW64699	Aaw64699 Seq ID 36
25	41	33.9	13	3	AAB23489	Aab23489 Activity
26	41	33.9	13	4	AAB72324	Aab72324 Activity
27	41	33.9	13	5	ABB07224	Abb07224 ADNF III
28	41	33.9	13	8	ADQ76132	Adq76132 ADNF III
29	41	33.9	13	8	ADQ76122	Adq76122 ADNF III
30	41	33.9	13	8	ADS73632	Ads73632 Elongated
31	41	33.9	14	8	ADS73617	Ads73617 ADNF III
32	41	33.9	14	8	ADS73631	Ads73631 Elongated
33	41	33.9	15	2	AAW64698	Aaw64698 Seq ID 35
34	41	33.9	15	3	AAB23490	Aab23490 Activity
35	41	33.9	15	4	AAB72325	Aab72325 Activity
36	41	33.9	15	5	ABB07225	Abb07225 ADNF III
37	41	33.9	15	8	ADQ76123	Adq76123 ADNF III
38	41	33.9	15	8	ADQ76133	Adq76133 ADNF III
39	41	33.9	15	8	ADS73618	Ads73618 ADNF III
40	41	33.9	18	2	AAW64680	Aaw64680 Human ADN
41	41	33.9	18	3	AAY71145	Aay71145 Inactive
42	41	33.9	18	3	AAB23491	Aab23491 Activity
43	41	33.9	18	4	AAB72326	Aab72326 Activity
44	41	33.9	18	5	ABB07226	Abb07226 ADNF III
45	41	33.9	18	8	ADQ76134	Adq76134 ADNF III

ALIGNMENTS

RESULT 1
AAW64677
ID   AAW64677 standard; protein; 8 AA.
XX
AC   AAW64677;
XX
DT   04-NOV-1998 (first entry)
XX
DE   Human ADNF-III peptide fragment.
XX
KW   Activity dependent neurotrophic factor III; ADNF-III; ADNP; cell death;
KW   activity dependent neuroprotective protein; neurone; excito-toxicity;
KW   spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;
KW   N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
KW   HIV infection.
XX
OS   Homo sapiens.
XX
PN   WO9835042-A2.
XX
PD   13-AUG-1998.
XX
PF   06-FEB-1998; 98WO-US002485.
XX
PR   07-FEB-1997; 97US-0037404P.
XX
PA   (USSH) US SEC HEALTH & HUMAN SERVICES.
XX
PI   Gozes I, Brenneman DE, Bassan M;
XX
PT   Activity dependent neurotrophic factor III polypeptide - useful
PT   therapeutically to prevent neuronal cell death associated with e.g. HIV
PT   infection, excito-toxicity or Alzheimer's disease.
XX
PS   Example 20; Page 75; 121pp; English.
XX
CC   This sequence represents a peptide used in a method which isolates a
CC   novel activity dependent neurotrophic factor III; ADNF-III (also known as
CC   activity dependent neuroprotective protein, ADNP). ADNF III polypeptides
CC   can be used to prevent neuronal cell death, of e.g. the spinal cord,
CC   hippocampal, cerebral cortical or cholinergic neurones associated with
CC   e.g. HIV infection, excito-toxicity induced by N-methyl-D-aspartate
CC   stimulation or beta-amyloid peptide in Alzheimer's disease. The
CC   polypeptides can also be combined with a carrier to alleviate learning
CC   impairment produced by cholingeric blockage in Alzheimer's patients. The
CC   nucleic acids are useful in polypeptide production and to detect ADNF III

WPI; 1998-447239/38.

CC polynucleotide in biological samples, while the antibodies are useful
CC therapeutically and to isolate ADNF III polypeptides
XX
SQ Sequence 8 AA;

Qy   41 NAPVSIPQ 48
        ||||||||
Db   1 NAPVSIPQ 8

Query Match   33.9%; Score 41; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
ID AAW64678 standard; protein; 8 AA.
XX
AC AAW64678;
XX
DT 04-NOV-1998 (first entry)
XX
DE Human ADNF-III derived active peptide #2.
XX
KW Activity dependent neurotrophic factor III; ADNF-III; ADNF; cell death;
KW activity dependent neuroprotective protein; neurone; excito-toxicity;
KW spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;
KW N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
KW HIV infection.
XX
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT Modified-site 1
FT   /note= "N-terminal Asn is modified by the presence of an
FT   (R1)x group where R1 is an amino acid sequence of 1 to 40
FT   amino acids wherein each amino acid is independently
FT   selected from a group consisting of naturally occurring
FT   amino acids and amino acid mimetics"
FT Modified-site 8
FT   /note= "C-terminal Gln is modified by the presence of an
FT   (R2)y group where R2 is an amino acid sequence of 1 to 40
FT   amino acids wherein each amino acid is independently
FT   selected from a group consisting of naturally occurring
FT   amino acids and amino acid mimetics"
XX
PN WO9835042-A2.
XX
PD 13-AUG-1998.
XX
PF 06-FEB-1998; 98WO-US002485.
PR 07-FEB-1997; 97US-0037404P.
XX
PA (USSH) US SEC HEALTH & HUMAN SERVICES.
XX
PI Gozes I, Brenneman DE, Bassan M;
XX
DR WPI; 1998-447239/38.
XX
PT Activity dependent neurotrophic factor III polypeptide - useful
PT therapeutically to prevent neuronal cell death associated with e.g. HIV
PT infection, excito-toxicity or Alzheimer's disease.
XX
PS Claim 24; Page 6; 121pp; English.
XX
CC This sequence represents a peptide used in a method which isolates a
CC novel activity dependent neurotrophic factor III. ADNF-III (also known as
CC activity dependent neuroprotective protein, ADNP). ADNF III polypeptides
CC can be used to prevent neuronal cell death, of e.g. the spinal cord,
CC hippocampal, cerebral cortical or cholinergic neurones associated with
CC e.g. HIV infection, excito-toxicity induced by N-methyl-D-aspartate
CC stimulation or beta-amyloid peptide in Alzheimer's disease. The

CC polypeptides can also be combined with a carrier to alleviate learning
CC impairment produced by cholinergic blockage in Alzheimer's patients. The
CC nucleic acids are useful in polypeptide production and to detect ADNF III
CC polynucleotide in biological samples, while the antibodies are useful
CC therapeutically and to isolate ADNF III polypeptides
XX
SQ Sequence 8 AA;

Qy   41 NAPVSIPQ 48
        ||||||||
Db   1 NAPVSIPQ 8

Query Match   33.9%; Score 41; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
ID AAY71143 standard; peptide; 8 AA.
XX
AC AAY71143;
XX
DT 08-SEP-2000 (first entry)
XX
DE Human ADNF III-8 or NAP peptide sequence, NAPVSIPQ.
XX
KW Activity Dependent Neurotrophic Factor III; ADNF; human; ADNF; NAP;
KW Activity Dependent Neuroprotective Protein; chromosome 20q13.2; ADNFLE;
KW autosomal dominant nocturnal frontal-lobe epilepsy; neuronal cell death;
KW neurological deficiency; treatment; HIV; human immunodeficiency virus;
KW Alzheimer's disease; beta-amyloid peptide; Huntington's disease;
KW epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;
KW amyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;
KW mitochondrial abnormality; Wernicke's encephalopathy; homocysteinuria;
KW hyperprolinemia; sulphite oxide disease; Tourette's syndrome; nootropic;
KW Down's syndrome; drug addiction; developmental retardation; antiepilepic;
KW learning impairment; anticonvulsant; neuroprotective; anti-HIV.
XX
OS Homo sapiens.
XX
PN WO200027875-A2.
XX
PD 18-MAY-2000.
XX
PF 04-NOV-1999; 99WO-US026213.
XX
PR 06-NOV-1998; 98US-0018730.
XX
PA (USAS) GOVERNMENT US REPRESENT AS.
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX
PI Gozes I, Brenneman DE, Bassan M, Zamostiano R;
XX
DR WPI; 2000-376491/32.
XX
PT New nucleic acid encoding an activity dependent neurotrophic factor III
PT (ADNF III) useful in the treatment of neurological deficiencies and for
PT preventing neuronal cell death.
XX
PS Example; Page 5; 136pp; English.
XX
CC The present sequence is the human Activity Dependent Neurotrophic Factor
CC (ADNF) III-8 or NAP peptide sequence. This peptide was synthesised based
CC on the structural homology to ADNF-9 active peptide and hsp60. It is also
CC used as an antigen for immunological detection of cloned ADNF III. ADNF
CC III is also called an Activity Dependent Neuroprotective Protein (ADNP).
CC The human gene was mapped to chromosome 20q13.2 and is linked to
CC autosomal dominant nocturnal frontal-lobe epilepsy (ADNFLE) gene. It is
CC expressed in the astrocytes, brain and also in foetal lung and endocrine
CC tissues. This sequence has homology to ADNF.I and hsp60, heat shock
CC protein and PIF1, a DNA repair protein. The ADNF III polypeptides are
CC useful for the treatment of neurological deficiencies and for prevention

CC   of neuronal cell death associated with gp120, the envelope protein from
CC   HIV; N-methyl-D-Aspartic acid (excito-toxicity); tetrodotoxin (blockage
CC   of electrical activity); and beta-amyloid peptide, a substance related to
CC   neuronal degeneration in Alzheimer's disease. It is useful for the
CC   treatment of Huntington's disease, AIDS dementia complex, epilepsy,
CC   neuropathic pain syndromes, Parkinson's disease, amyotrophic lateral
CC   sclerosis (ALS), mitochondrial abnormalities, Leber's disease, Wernicke's
CC   encephalopathy, Alzheimer's disease, homocysteinuria, hyperprolinemia,
CC   sulphite oxide disease, Tourette's syndrome, oxidative stress induced
CC   neuronal death, Down's syndrome, developmental retardation and learning
CC   impairments, drug addiction, tolerance and dependency
XX
SQ   Sequence 8 AA;

Qy   41 NAPVSIPQ 48
        ||||||||
Db   1 NAPVSIPQ 8

Query Match   33.9%; Score 41; DB 3; Length 8;
Best Local Similarity   100.0%; Pred. No. 1.8e+06;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 4
AAB23470
ID   AAB23470 standard; peptide; 8 AA.
XX
AC   AAB23470;
XX
DT   22-JAN-2001 (first entry)
XX
DE   Activity dependent neurotrophic factor I peptide #2.
XX
KW   Activity dependent neurotrophic factor; ADNF; FAS;
KW   foetal alcohol syndrome; gene therapy; neurological deficiency;
KW   neuronal cell death.
OS   Unidentified.
XX
PN   WO200053217-A2.
XX
PD   14-SEP-2000.
XX
PF   10-MAR-2000; 2000WO-US006364.
XX
PR   12-MAR-1999; 99US-0026751l.
XX
PA   (UYRA-) UNIV RAMOT.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Brenneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;
XX
DR   WPI; 2000-601940/57.
XX
PT   Claim 9; Page 51; 65pp; English.
PT
PT   Treating condition associated with fetal alcohol syndrome in a subject
PT   exposed to alcohol in utero or reducing neuronal death, involves
PT   administering activity dependent neurotrophic factors I and/or III.
CC
CC   The present invention relates to the treatment of a condition associated
CC   with foetal alcohol syndrome (FAS), involving administering an activity
CC   dependent neurotropic factor (ADNF). ADNFs of the present invention may
CC   also be used to treat neurological deficiencies and prevent neuronal cell
CC   death. The present sequence is an ADNF peptide
XX
SQ   Sequence 8 AA;

Qy   41 NAPVSIPQ 48
        ||||||||
Db   1 NAPVSIPQ 8

RESULT 5
AAB23472
ID   AAB23472 standard; peptide; 8 AA.
XX
AC   AAB23472;
XX
DT   22-JAN-2001 (first entry)
XX
DE   Activity dependent neurotrophic factor I peptide #4.
XX
KW   Activity dependent neurotrophic factor; ADNF; FAS;
KW   foetal alcohol syndrome; gene therapy; neurological deficiency;
KW   neuronal cell death.
OS   Unidentified.
XX
PN   WO200053217-A2.
XX
PD   14-SEP-2000.
XX
PF   10-MAR-2000; 2000WO-US006364.
XX
PR   12-MAR-1999; 99US-00267511.
XX
PA   (UYRA-) UNIV RAMOT.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Brenneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;
XX
DR   WPI; 2000-601940/57.
XX
PT   Disclosure; Page 51; 65pp; English.
PT
PT   Treating condition associated with fetal alcohol syndrome in a subject
PT   exposed to alcohol in utero or reducing neuronal death, involves
CC   administering activity dependent neurotrophic factors I and/or III.
CC
CC   The present invention relates to the treatment of a condition associated
CC   with foetal alcohol syndrome (FAS), involving administering an activity
CC   dependent neurotropic factor (ADNF). ADNFs of the present invention may
CC   also be used to treat neurological deficiencies and prevent neuronal cell
CC   death. The present sequence is an ADNF peptide
XX
SQ   Sequence 8 AA;

Qy   41 NAPVSIPQ 48
        ||||||||
Db   1 NAPVSIPQ 8

Query Match   33.9%; Score 41; DB 3; Length 8;
Best Local Similarity   100.0%; Pred. No. 1.8e+06;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 6
AAB72322
ID   AAB72322 standard; peptide; 8 AA.
XX
AC   AAB72322;
XX
DT   16-MAY-2001 (first entry)
XX
DE   Activity dependent neurotrophic factor III (ADNF III) peptide SEQ ID 2.
XX
KW   Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;
KW   neuronal cell death; Alzheimer's disease; oxidative stress; VIP;
KW   vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.
OS   Synthetic.

```
XX
PN  WO200112654-A2
XX
PD  22-FEB-2001.
XX
PF  17-AUG-2000; 2000WO-US022861.
XX
PR  18-AUG-1999; 99US-0149956P.
XX
PA  (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Brenneman DE, Gozes I, Spong CY, Pinhasov A, Giladi E;
XX
DR  WPI; 2001-202855/20.
XX
PS  Claim 10; Page 57; 88pp; English.
XX
PT  Novel Activity Dependent Neurotrophic Factor I useful for treating
PT  oxidative stress, reducing neuronal cell death and treating a condition
PT  associated with fetal alcohol syndrome.
XX
CC  This invention relates to an activity dependent neurotrophic factor I
CC  (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72321 represent
CC  ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent
CC  ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical
CC  composition containing either ADNF I or ADNF III are useful for reducing
CC  neuronal cell death, e.g. death of spinal cord neurons, hippocampal
CC  neurons, cerebral cortical neurons and cholinergic neurons, in a patient
CC  infected with a virus, e.g. human immunodeficiency virus (HIV). The
CC  neuronal cell death is associated with excito-toxicity induced by N-
CC  methyl-D-aspartate (NMDE) stimulation, which is induced by beta-amyloid
CC  peptide in an Alzheimer's disease patient, or induced by cholinergic
CC  blockade. ADNF I, ADNF III and the pharmaceutical composition are also
CC  useful for treating oxidative stress in a patient, for reducing a
CC  condition, such as decreased body weight, decreased brain weight,
CC  decreased level of vasoactive intestinal peptide (VIP) mRNA, and foetal
CC  death, associated with foetal alcohol syndrome
XX
SQ  Sequence 8 AA;

Qy  41 NAPVSIPQ 48
        ||||||||
Db   1 NAPVSIPQ 8

Query Match    33.9%;   Score 41;  DB 4;  Length 8;
Best Local Similarity   100.0%;   Pred. No. 1.8e+06;
Matches   8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;


RESULT 7
ID  ABB07216 standard; peptide; 8 AA.
XX
AC  ABB07216;
XX
DT  26-MAR-2002  (first entry)
XX
DE  ADNF III polypeptide active core site peptide sequence.
XX
KW  ADNF; Activity Dependent Neurotrophic Factor; nootropic; neuroprotective;
KW  cerebroprotective; antidiabetic; neuroleptic; anticonvulsant; anti-HIV;
KW  antiparkinsonian; tranquilizer; antialcoholic; vulnerary; antibacterial;
KW  antiinflammatory; antidote; ophthalmological; muscular; vasodilator;
KW  NMDA receptor.
XX
OS  Synthetic.
XX
PN  WO200192333-A2.
XX
PD  06-DEC-2001.
XX
PF  31-MAY-2001; 2001WO-US017758.
```

```
XX
PR  31-MAY-2000; 2000US-0208944P.
PR  08-FEB-2001; 2001US-0267805P.
XX
PA  (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Spong CY, Brenneman D, Gozes I;
XX
DR  WPI; 2002-114330/15.
XX
PS  Claim 1; Page 51; 80pp; English.
XX
PT  Use of an activity dependent neurotrophic factor for improving learning
PT  and/or memory in a subject by pre- or post-natal administration.
XX
CC  The invention provides a method of improving learning and/or memory in a
CC  subject that involves administering pre- or postnatally an Activity
CC  Dependent Neurotrophic Factor (ADNF) to the subject. The ADNF polypeptide
CC  is an ADNF I and/or an ADNF III polypeptide comprising the core active
CC  site sequences ABB07215 or ABB07216. The method is useful for improving
CC  learning and/or memory in a subject; for treating a normal or old subject
CC  afflicted with neuropathology, Alzheimer's disease, Down's syndrome,
CC  normal mental capacity, mental retardation, for the treatment of central
CC  motor systems including degenerative conditions affecting the basal
CC  ganglia (see ABB07215 for a detailed description of the various
CC  conditions that can be treated by using the ADNF polypeptides). The
CC  present sequence represents the active core site sequence of the ADNF III
CC  polypeptide
XX
SQ  Sequence 8 AA;

Qy  41 NAPVSIPQ 48
        ||||||||
Db   1 NAPVSIPQ 8

Query Match    33.9%;   Score 41;  DB 5;  Length 8;
Best Local Similarity   100.0%;   Pred. No. 1.8e+06;
Matches   8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;


RESULT 8
ID  ABR39742 standard; peptide; 8 AA.
XX
AC  ABR39742;
XX
DT  23-JUN-2003  (first entry)
XX
DE  ADNF I active core peptide fragment NAP.
XX
KW  ADNF I; Activity Dependent Neurotrophic Factor I; neuroprotective;
KW  anti-HIV; neuroleptic; antiparkinsonian; nootropic; ADNP; NAP; SAL;
KW  Activity Dependent Neuroprotective Protein.
XX
OS  Unidentified.
XX
PN  WO200302226-A2.
XX
PD  20-MAR-2003.
XX
PF  12-SEP-2002; 2002WO-US029146.
XX
PR  12-SEP-2001; 2001US-0322760P.
PR  10-APR-2002; 2002US-0371961P.
XX
PA  (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Brenneman DE, Castellon R, Spong CY, Hauser JM, Gozes I;
XX
DR  WPI; 2003-354501/33.
XX
```

PT New Activity Dependent Neurotrophic Factor I complex polypeptide, useful
PT for reducing neuronal cell death, treating oxidative stress in a patient,
PT or improving learning and/or memory in a subject with e.g. Alzheimer's
PT disease.

XX
PS Disclosure; Page 2; 111pp; English.
XX
CC The invention relates to Activity Dependent Neurotrophic Factor I (ADNF
CC I) complex polypeptide selected from sequences AAR39744-754. The ADNF I
CC complex polypeptide is useful for reducing neuronal cell death in
CC conditions such as HIV infection, treating oxidative stress in a patient,
CC reducing a condition associated with fetal alcohol syndrome, or improving
CC learning and/or memory in a subject with e.g. Alzheimer's disease or
CC Down's syndrome. The ADNF complex polypeptides are also useful in
CC designing a drug treatment regime that can be individually tailored for
CC each patient affected by neurodegenerative disorders. The polypeptides
CC can also be used for diagnosing or treating Huntington's disease,
CC Wilson's disease, Parkinson's disease, AIDS-related dementia or
CC Tourette's syndrome. The present sequence represents a ADNP (activity
CC dependent neuroprotective protein) peptide, that has a biological
CC activity similar to a ADNF I peptide SAL.
XX
SQ Sequence 8 AA;

Query Match   33.9%; Score 41; DB 6; Length 8;
Best Local Similarity   100.0%; Pred. No. 1.8e+06;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
               ||||||||
Db   1 NAPVSIPQ 8

RESULT 9
AC ADA07953
ID ADA07953 standard; peptide; 8 AA.
XX
AC ADA07953;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human activity dependent neuroprotective factor (ADNP) peptide #2.
XX
KW Human; glaucomatous optic neuropathy;
KW activity dependent neuroprotective factor; ADNP; ophthalmological.
XX
OS Homo sapiens.
XX
PN US2003166544-A1.
XX
PD 04-SEP-2003.
XX
PF 06-JUN-2002; 2002US-0016432.
PR 07-SEP-2000; 2000US-0230964P.
PR 02-AUG-2001; 2001US-0092029.
XX
PA (CLAR/) CLARK A F.
PA (SHAD/) SHADE D L.
XX
PI Clark AF, Shade DL;
XX
DR WPI; 2003-720933/68.
XX
PT Treating glaucomatous optic neuropathy by administering a composition
PT comprising a peptide derived from or related to Activity Dependent
PT Neuroprotective Factor (ADNP).
XX
PS Claim 2; Page 2; 13pp; English.
XX
CC The present invention relates to a method for preventing and treating
CC glaucomatous optic neuropathy. The method comprises administering a
CC composition comprising a peptide derived from activity dependent

---

CC neuroprotective factor (ADNP). The method is useful for treating
CC glaucomatous optic neuropathy. The present sequence represents a peptide
CC from human ADNP.
XX
SQ Sequence 8 AA;

Query Match   33.9%; Score 41; DB 7; Length 8;
Best Local Similarity   100.0%; Pred. No. 1.8e+06;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
               ||||||||
Db   1 NAPVSIPQ 8

RESULT 10
AC ADQ76121
ID ADQ76121 standard; peptide; 8 AA.
XX
AC ADQ76121;
XX
DT 07-OCT-2004 (first entry)
XX
DE ADNF III active core site peptide SEQ ID NO:2.
XX
KW activity dependent neurotropic factor; ADNF; ADNF III; active core site;
KW immunosuppressive; nootropic; neuroprotective; antiinflammatory;
KW vasotropic; muscular; CNS; thyromimetic; antithyroid; antirheumatic;
KW antiarthritic; hepatotropic; virucide; dermatological; haemostatic;
KW antidiabetic; antibacterial; neurotropic factor agonist;
KW autoimmune disease; multiple sclerosis; myasthenia gravis;
KW Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;
KW Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;
KW hypothyroiditis; primary biliary cirrhosis;
KW mixed connective tissue disease; chronic active hepatitis;
KW Graves' disease; hyperthyroiditis; scleroderma;
KW chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;
KW septic shock.
XX
OS Synthetic.
XX
PN WO200406309-A2.
XX
PD 22-JUL-2004.
XX
PF 30-DEC-2003; 2003WO-US041540.
XX
PR 02-JAN-2003; 2003US-0437650P.
XX
PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Gozes I, Offen D, Giladi E, Melamed E, Brenneman D;
XX
DR WPI; 2004-543782/52.
XX
PT Preventing or treating autoimmune diseases, such as multiple sclerosis,
PT rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic
PT shock, using an Activity Dependent Neurotropic Factor (ADNF) polypeptide.
XX
PS Claim 1; SEQ ID NO 2; 39pp; English.
XX
CC The present invention describes a method for preventing or treating an
CC autoimmune disease in a subject. The method comprises administering an
CC activity dependent neurotropic factor (ADNF) polypeptide, where the ADNF
CC polypeptide is a member selected from the group consisting of: (a) an
CC ADNF I polypeptide comprising an active core site with the amino acid
CC sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide
CC comprising an active core site with the amino acid sequence of SEQ ID
CC NO:2 (ADQ76121); and (c) a mixture of the ADNF I polypeptide of part (a)
CC and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
CC host cells, vectors and antibodies used in the methods are also disclosed
CC in the present invention. ADNF sequences have immunosuppressive,

RESULT 11

ID   ADS73609 standard; peptide; 8 AA.
XX
AC   ADS73609;
XX
DT   16-DEC-2004 (first entry)
XX
DE   ADNF III active core site.
XX
KW   active; core peptide; Activity Dependent Neurotrophic Factor; ADNF;
KW   ADNF I; ADNF III; anxiety; depression; lipophilic moiety; penetration;
KW   activity; panic disorder; obsessive-compulsive disorder;
KW   post-traumatic stress disorder; social phobia; social anxiety disorder;
KW   specific phobia; generalized anxiety disorder; Major depression;
KW   dysthymia; bipolar disorder; NAP-tubulin; binding site; anxiolytic drug;
KW   neuroprotection.
XX
OS   Homo sapiens.
XX
PN   WO2004080957-A2.
XX
PD   23-SEP-2004.
XX
PF   11-MAR-2004; 2004WO-II000232.
XX
PR   12-MAR-2003; 2003US-0454505P.
XX
PA   (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
XX
PI   Gozes I, Alcalay RN, Divinski I, Giladi E;
XX
DR   WPI; 2004-668930/65.
XX
PT   Treating or preventing anxiety or depression in a subject comprises
PT   administering an amount of an Activity Dependent Neurotrophic Factor
PT   polypeptide to the subject.
XX
PS   Claim 2; SEQ ID NO 2; 46pp; English.
XX
CC   This sequence represents the active core peptide derived from Activity
CC   Dependent Neurotrophic Factor (ADNF) III. This peptide may be used for
CC   treating or preventing anxiety or depression in a subject. This sequence
CC   may optionally be extended at either the N- and/or the C-terminals. The
CC   ADNF polypeptide of the invention may be encoded by a nucleic acid that
CC   is administered to the subject. It also contains a covalently bound
CC   lipophilic moiety to enhance penetration or activity. The subject suffers
CC   from anxiety or depression and the ADNF polypeptide is administered to
CC   prevent anxiety or depression. The disease is selected from a panic
CC   disorder, obsessive-compulsive disorder, post-traumatic stress disorder,
CC   social phobia, social anxiety disorder, specific phobias, generalized
CC   anxiety disorder, Major depression, dysthymia, and bipolar disorder. The
CC   NAP-tubulin binding site(s) is/are used to identify anxiolytic drugs and
CC   drugs that alleviate depression and provide neuroprotection.

Qy   Sequence 8 AA;

Db

Query Match   33.9%;   Score 41; DB 8; Length 8;
Best Local Similarity 100.0%;   Pred. No. 1.8e+06;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
                |||||||
Db   1 NAPVSIPQ 8

RESULT 12

ID   AAW64696 standard; protein; 10 AA.
XX
AC   AAW64696;
XX
DT   17-OCT-2003 (revised)
DT   04-NOV-1998 (first entry)
XX
DE   Seq ID 33 from WO9835042.
XX
KW   Activity dependent neurotrophic factor III; ADNF-III; ADNP; cell death;
KW   activity dependent neuroprotective protein; neurone; excito-toxicity;
KW   spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;
KW   N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
KW   HIV infection.
XX
OS   unidentified.
XX
PN   WO9835042-A2.
XX
PD   13-AUG-1998.
XX
PF   06-FEB-1998; 98WO-US002485.
XX
PR   07-FEB-1997; 97US-0037404P.
XX
PA   (USSH) US SEC HEALTH & HUMAN SERVICES.
XX
PI   Gozes I, Brenneman DE, Bassan M;
XX
DR   WPI; 1998-447239/38.
XX
PT   Activity dependent neurotrophic factor III polypeptide - useful
PT   therapeutically to prevent neuronal cell death associated with e.g. HIV
PT   infection, excito-toxicity or Alzheimer's disease.
XX
PS   Disclosure; Page; 121pp; English.
XX
CC   This specification describes the isolation of novel activity dependent
CC   neurotrophic factor III, ADNF-III (also known as activity dependent
CC   neuroprotective protein, ADNP) sequences. ADNF III polypeptides can be
CC   used to prevent neuronal cell death, of e.g. the spinal cord,
CC   hippocampal, cerebral cortical or cholinergic neurones associated with
CC   e.g. HIV infection, excito-toxicity induced by N-methyl-D-aspartate
CC   stimulation or beta-amyloid peptide in Alzheimer's disease. The
CC   polypeptides can also be combined with a carrier to alleviate learning
CC   impairment produced by cholinergic blockage in Alzheimer's patients. The
CC   nucleic acids are useful in polypeptide production and to detect ADNF III
CC   polynucleotide in biological samples, while the antibodies are useful
CC   therapeutically and to isolate ADNF III polypeptides. NOTE: This sequence
CC   does not appear in the specification but is present in the Sequence ID
CC   listing. (Updated on 17-OCT-2003 to standardise OS field)

Qy   Sequence 8 AA;

Db

Query Match   33.9%;   Score 41; DB 8; Length 8;
Best Local Similarity 100.0%;   Pred. No. 1.8e+06;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
                |||||||
Db   1 NAPVSIPQ 8

CC   nootropic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
CC   thyromimetic, antithyroid, antirheumatic, antiarthritic, hepatotropic,
CC   vincide, dermatological, haemostatic, antidiabetic and antibacterial
CC   activities, and can be used as neurotropic factor agonists. The methods
CC   and compositions of the present invention are useful for the prevention
CC   and/or treatment of autoimmune diseases, such as multiple sclerosis,
CC   myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,
CC   Behcet's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
CC   disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
CC   tissue disease, chronic active hepatitis, Graves'
CC   disease/hyperthyroiditis, scleroderma, chronic idiopathic
CC   thrombocytopenic purpura, diabetic neuropathy and septic shock. The
CC   present sequence represents an ADNF III active core site peptide from the
CC   present invention.
XX
SQ   Sequence 8 AA;

Qy   Sequence 8 AA;

Db

Query Match   33.9%;   Score 41; DB 8; Length 8;
Best Local Similarity 100.0%;   Pred. No. 1.8e+06;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
                |||||||
Db   1 NAPVSIPQ 8

SQ   Sequence 10 AA;

Query Match   33.9%; Score 41; DB 2; Length 10;
Best Local Similarity   100.0%; Pred. No. 0.32;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
              ||||||||
Db   3 NAPVSIPQ 10

RESULT 13
AAY71139
ID   AAY71139 standard; peptide; 10 AA.
XX
AC   AAY71139;
XX
DT   08-SEP-2000 (first entry)
XX
DE   Human Activity Dependent Neurotrophic Factor (ADNF) III generic peptide.
XX
KW   Activity Dependent Neurotrophic Factor III; ADNF; human; ADNP;
KW   Activity Dependent Neuroprotective Protein; chromosome 20q13.2; ADNFLE;
KW   autosomal dominant nocturnal frontal-lobe epilepsy; neuronal cell death;
KW   neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;
KW   Alzheimer's disease; beta-amyloid peptide; Huntington's disease;
KW   epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;
KW   amyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;
KW   mitochondrial abnormality; Wernicke's encephalopathy; homocysteinuria;
KW   hyperprolinemia; sulphite oxide disease; Tourette's syndrome; nootropic;
KW   Down's syndrome; drug addiction; developmental retardation; antilipemic;
KW   learning impairment; anticonvulsant; neuroprotective; anti-HIV.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   Misc-difference 1
FT   /note= "Xaa= (R1)x= N-terminal amino acid sequence
FT   comprising 1-40 residues, where x= one or zero"
FT   Misc-difference 10
FT   /note= "Xaa= (R2)y= C-terminal amino acid sequence
FT   comprising 1-40 residues, where y= one or zero"
XX
PN   WO200027875-A2.
XX
PD   18-MAY-2000.
XX
PF   04-NOV-1999; 99WO-US026213.
XX
PR   06-NOV-1998; 98US-00187330.
XX
PA   (USAS) GOVERNMENT US REPRESENT AS.
PA   (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX
PI   Gozes I, Brenneman DE, Bassan M, Zamostiano R;
XX
DR   WPI; 2000-376491/32.
XX
PT   New nucleic acid encoding an activity dependent neurotrophic factor III
PT   (ADNF III) useful in the treatment of neurological deficiencies and for
PT   preventing neuronal cell death.
XX
PS   Claim 25; Page 95; 136pp; English.
XX
CC   The present sequence is the human Activity Dependent Neurotrophic Factor
CC   (ADNF) III generic peptide. It consists of the ADNF III-8 or NAP peptide,
CC   flanked by N- and C-terminal generic sites, comprising 1-40 amino acids.
CC   ADNF III is also called an Activity Dependent Neuroprotective Protein
CC   (ADNP). The human gene was mapped to chromosome 20q13.2 and is linked to
CC   autosomal dominant nocturnal frontal-lobe epilepsy (ADNFLE) gene. It is
CC   expressed in the astrocytes, brain and also in foetal lung and endocrine
CC   tissues. This sequence has homology to ADNF I and hsp60, heat shock
CC   protein and PIF1, a DNA repair protein. The ADNF III polypeptides are

CC   useful for the treatment of neurological deficiencies and for prevention
CC   of neuronal cell death associated with gp120, the envelope protein from
CC   HIV; N-methyl-D-Aspartic acid (excito-toxicity); tetrodotoxin (blockage
CC   of electrical activity); and beta-amyloid peptide, a substance related to
CC   neuronal degeneration in Alzheimer's disease. It is useful for the
CC   treatment of Huntington's disease, Parkinson's disease, amyotrophic
CC   neuropathic pain syndromes, AIDS dementia complex, epilepsy,
CC   sclerosis (ALS), mitochondrial abnormalities, Leber's disease, Wernicke's
CC   encephalopathy, Alzheimer's disease, homocysteinuria, hyperprolinemia,
CC   sulphite oxide disease, Tourette's syndrome, oxidative stress induced
CC   neuronal death, Down's syndrome, developmental retardation and learning
CC   impairments, drug addiction, tolerance and dependency
XX
SQ   Sequence 10 AA;

Query Match   33.9%; Score 41; DB 3; Length 10;
Best Local Similarity   100.0%; Pred. No. 0.32;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
              ||||||||
Db   2 NAPVSIPQ 9

RESULT 14
AAB23488
ID   AAB23488 standard; peptide; 10 AA.
XX
AC   AAB23488;
XX
DT   14-MAY-2003 (revised)
DT   22-JAN-2001 (first entry)
XX
DE   Activity dependent neurotrophic factor III peptide #1.
XX
KW   Activity dependent neurotrophic factor; ADNF; FAS;
KW   foetal alcohol syndrome; gene therapy; neurological deficiency;
KW   neuronal cell death.
XX
OS   Unidentified.
XX
PN   WO200053217-A2.
XX
PD   14-SEP-2000.
XX
PF   10-MAR-2000; 2000WO-US006364.
XX
PR   12-MAR-1999; 99US-00267511.
XX
PA   (UYRA-) UNIV RAMOT.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Brenneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;
XX
DR   WPI; 2000-601940/57.
XX
PT   Treating condition associated with fetal alcohol syndrome in a subject
PT   exposed to alcohol in utero or reducing neuronal death, involves
PT   administering activity dependent neurotrophic factors I and/or III.
XX
PS   Claim 10; Page 4; 65pp; English.
XX
CC   The present invention relates to the treatment of a condition associated
CC   with foetal alcohol syndrome (FAS), involving administering an activity
CC   dependent neurotrophic factor (ADNF). ADNFs of the present invention may
CC   also be used to treat neurological deficiencies and prevent neuronal cell
CC   death. The present sequence is an ADNF peptide. (Updated on 14-MAY-2003
CC   to correct PS field.)
XX
SQ   Sequence 10 AA;

Query Match   33.9%; Score 41; DB 3; Length 10;
Best Local Similarity   100.0%; Pred. No. 0.32;

```
Qy          41 NAPVSIPQ 48
            ||||||||||
Db           3 NAPVSIPQ 10

Matches     8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;     Job time : 119.825 secs


RESULT 15
AAB72323
ID   AAB72323 standard; peptide; 10 AA.
XX
AC   AAB72323;
XX
DT   16-MAY-2001  (first entry)
XX
DE   Activity dependent neurotrophic factor III (ADNF III) peptide SEQ ID 17.
XX
KW   Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;
KW   neuronal cell death; Alzheimer's disease; oxidative stress; VIP;
KW   vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.
XX
OS   Synthetic.
XX
PN   WO200112654-A2.
XX
PD   22-FEB-2001.
XX
PF   17-AUG-2000; 2000WO-US022861.
XX
PR   18-AUG-1999;  99US-0149956P.
XX
PA   (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Brenneman DE, Gozes I, Spong CY, Pinhasov A, Giladi E;
XX
DR   WPI; 2001-202855/20.
XX
PT   Novel Activity Dependent Neurotrophic Factor I useful for treating
PT   oxidative stress, reducing neuronal cell death and treating a condition
PT   associated with fetal alcohol syndrome.
XX
PS   Claim 16; Page 57; 88pp; English.
XX
CC   This invention relates to an activity dependent neurotrophic factor I
CC   (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72321 represent
CC   ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent
CC   ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical
CC   composition containing either ADNF I or ADNF III are useful for reducing
CC   neuronal cell death, e.g. death of spinal cord neurons, hippocampal
CC   neurons, cerebral cortical neurons and cholinergic neurons, in a patient
CC   infected with a virus, e.g. human immunodeficiency virus (HIV). The
CC   neuronal cell death is associated with excito-toxicity induced by N-
CC   methyl-D-aspartate (NMDA) stimulation, which is induced by beta-amyloid
CC   peptide in an Alzheimer's disease patient, or induced by cholinergic
CC   blockade. ADNF I, ADNF III and the pharmaceutical composition are also
CC   useful for treating oxidative stress in a patient, for reducing a
CC   condition, such as decreased body weight, decreased brain weight,
CC   decreased level of vasoactive intestinal peptide (VIP) mRNA, and foetal
CC   death, associated with foetal alcohol syndrome
XX
SQ   Sequence 10 AA;

Query Match             33.9%;  Score 41;  DB 4;  Length 10;
Best Local Similarity  100.0%;  Pred. No. 0.32;
Matches    8;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          41 NAPVSIPQ 48
            ||||||||||
Db           3 NAPVSIPQ 10


Search completed: February 23, 2005, 19:30:08
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: February 23, 2005, 19:23:02 ; Search time 29.8305 Seconds
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                   4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                   5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	41	33.9	8	4	US-09-187-330-6	Sequence 6, Appli
2	41	33.9	10	4	US-09-187-330-33	Sequence 33, Appl
3	41	33.9	13	4	US-09-187-330-34	Sequence 34, Appl
4	41	33.9	15	4	US-09-187-330-35	Sequence 35, Appl
5	41	33.9	18	4	US-09-187-330-12	Sequence 12, Appl
6	41	33.9	88	4	US-09-187-330-10	Sequence 10, Appl
7	41	33.9	726	4	US-09-187-330-57	Sequence 57, Appl
8	41	33.9	781	4	US-09-187-330-32	Sequence 32, Appl
9	41	33.9	787	4	US-09-187-330-31	Sequence 31, Appl
10	41	33.9	800	4	US-09-187-330-41	Sequence 41, Appl
11	41	33.9	806	4	US-09-187-330-3	Sequence 3, Appl
12	41	33.9	828	4	US-09-187-330-55	Sequence 55, Appl
13	41	33.9	874	4	US-09-187-330-59	Sequence 59, Appl
14	41	33.9	1000	4	US-09-187-330-1	Sequence 1, Appl
15	41	33.9	1102	4	US-09-364-609-8	Sequence 8, Appli
16	36	29.8	9	4	US-09-187-330-28	Sequence 28, Appl
17	36	29.8	360	4	US-09-252-991A-31993	Sequence 31993, A
18	36	29.8	510	4	US-09-634-238-237	Sequence 237, App
19	36	29.8	519	4	US-09-134-000C-6226	Sequence 6226, Ap
20	34	28.1	469	4	US-09-328-352-4822	Sequence 4822, Ap
21	34	28.1	469	4	US-09-949-016-9522	Sequence 9522, Ap
22	33	27.3	205	4	US-09-489-039A-7548	Sequence 7548, Ap
23	33	27.3	481	4	US-09-489-039A-9148	Sequence 9148, Ap
24	31	25.6	114	4	US-09-270-767-33696	Sequence 33696, A
25	31	25.6	114	4	US-09-270-767-48911	Sequence 48911, A
26	31	25.6	292	4	US-09-328-352-8057	Sequence 8057, Ap
27	31	25.6	306	4	US-09-248-796A-24473	Sequence 24473, A
28	31	25.6	317	4	US-09-543-681A-4789	Sequence 4789, Ap
29	31	25.6	376	4	US-09-489-039A-7535	Sequence 7535, Ap
30	31	25.6	392	4	US-09-600-099-6	Sequence 6, Appli
31	31	25.6	444	4	US-09-902-540-12378	Sequence 12378, A
32	31	25.6	459	6	US-09-194375-6	Patent No. 5194375
33	31	25.6	459	6	US-09-194375-6	Patent No. 5194375
34	31	25.6	521	4	US-09-710-279-532	Sequence 532, App
35	31	25.6	525	3	US-09-134-001C-3514	Sequence 3514, Ap
36	31	25.6	881	1	US-08-333-901-1	Sequence 1, Appli
37	31	25.6	881	2	US-08-456-582-1	Sequence 1, Appli
38	31	25.6	881	2	US-08-898-789-1	Sequence 1, Appli
39	31	25.6	881	4	US-09-039-555B-16	Sequence 16, Appl
40	31	25.6	951	3	US-08-324-258-7	Sequence 7, Appli
41	31	25.6	951	4	US-08-816-346-58	Sequence 58, Appl
42	31	25.6	951	4	US-09-335-411-58	Sequence 58, Appl
43	31	25.6	952	2	US-08-788-674-5	Sequence 5, Appli
44	31	25.6	952	3	US-08-816-346-4	Sequence 4, Appli
45	31	25.6	952	3	US-09-335-411-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-187-330-6

Sequence 6, Application US/09187330

; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-29120OUS
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III-8
; OTHER INFORMATION: active site core peptide, clone 25 sequence (NAP)
US-09-187-330-6

Query Match   33.9%; Score 41; DB 4; Length 8;
Best Local Similarity   100.0%;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
               ||||||||
Db   1 NAPVSIPQ 8

RESULT 2
US-09-187-330-33

Sequence 33, Application US/09187330

; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America

```
;  APPLICANT: as represented by the Secretary of the
;  APPLICANT: Department of Health and Human Services
;  TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
;  FILE REFERENCE: 015280-29120US
;  CURRENT APPLICATION NUMBER: US/09/187,330
;  CURRENT FILING DATE: 1998-11-06
;  EARLIER APPLICATION NUMBER: US 60/037,404
;  EARLIER FILING DATE: 1997-02-07
;  EARLIER APPLICATION NUMBER: WO PCT/US98/02485
;  EARLIER FILING DATE: 1998-02-06
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn Ver. 2.0
;
;  SEQ ID NO 33
;  LENGTH: 10
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence:ADNF III
;  OTHER INFORMATION: polypeptide
US-09-187-330-33

Qy    41 NAPVSIPQ 48
         ||||||||
Db     3 NAPVSIPQ 10


RESULT 3
US-09-187-330-34
Sequence 34, Application US/09187330
Patent No. 6613740
GENERAL INFORMATION:
APPLICANT: Gozes, Illana
APPLICANT: Brenneman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamostiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-29120US
CURRENT APPLICATION NUMBER: US/09/187,330
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/037,404
EARLIER FILING DATE: 1997-02-07
EARLIER APPLICATION NUMBER: WO PCT/US98/02485
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III
OTHER INFORMATION: polypeptide
US-09-187-330-34

Query Match      33.9%;  Score 41;  DB 4;  Length 13;
Best Local Similarity   100.0%;  Pred. No. 0.14;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    41 NAPVSIPQ 48
         ||||||||
Db     4 NAPVSIPQ 11


RESULT 4
US-09-187-330-35
; Sequence 35, Application US/0918730
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```
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-29120US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 35
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-187-330-35

Query Match      33.9%;  Score 41;  DB 4;  Length 15;
Best Local Similarity   100.0%;  Pred. No. 0.17;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    41 NAPVSIPQ 48
         ||||||||
Db     6 NAPVSIPQ 13


RESULT 5
US-09-187-330-12
Sequence 12, Application US/09187330
Patent No. 6613740
GENERAL INFORMATION:
APPLICANT: Gozes, Illana
APPLICANT: Brenneman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamostiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-29120US
CURRENT APPLICATION NUMBER: US/09/187,330
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/037,404
EARLIER FILING DATE: 1997-02-07
EARLIER APPLICATION NUMBER: WO PCT/US98/02485
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III
OTHER INFORMATION: polypeptide
US-09-187-330-12

Query Match      33.9%;  Score 41;  DB 4;  Length 18;
Best Local Similarity   100.0%;  Pred. No. 0.2;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    41 NAPVSIPQ 48
```

Db
```
  9 NAPVSIPQ 16
    ||||||||
```

RESULT 6
US-09-187-330-10
; Sequence 10, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-29120US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 10
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:activity
; OTHER INFORMATION: dependent neurotrophic factor III (ADNF III)
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(40)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-40 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (49)..(88)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 49-88 may be
; OTHER INFORMATION: present or absent
US-09-187-330-10

```
Qy  41 NAPVSIPQ 48
       ||||||||
Db  41 NAPVSIPQ 48
```

Query Match 33.9%; Score 41; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
US-09-187-330-57
; Sequence 57, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-29120US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 57
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-187-330-57

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Qy  41 NAPVSIPQ 48
       ||||||||
Db  59 NAPVSIPQ 66
```

Query Match 33.9%; Score 41; DB 4; Length 726;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-09-187-330-32
; Sequence 32, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-29120US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 32
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human activity dependent neurotrophic factor III
; OTHER INFORMATION: (ADNF III)
US-09-187-330-32

```
Qy  41 NAPVSIPQ 48
       ||||||||
Db  33 NAPVSIPQ 40
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Query Match 33.9%; Score 41; DB 4; Length 781;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
US-09-187-330-31
; Sequence 31, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-29120US

; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; OTHER INFORMATION: (ADNF III)
US-09-187-330-31

SEQ ID NO 31
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse activity dependent neurotrophic factor III

Qy   41 NAPVSIPQ 48
          ||||||||
Db   33 NAPVSIPQ 40

Query Match   33.9%;   Score 41;   DB 4;   Length 787;
Best Local Similarity   100.0%;   Pred. No. 11;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 10
US-09-187-330-41
; Sequence 41, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
US-09-187-330-41

SEQ ID NO 41
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(800)
; OTHER INFORMATION: translation of H3' human ADNF III cDNA clone

Qy   41 NAPVSIPQ 48
          ||||||||
Db   52 NAPVSIPQ 59

Query Match   33.9%;   Score 41;   DB 4;   Length 800;
Best Local Similarity   100.0%;   Pred. No. 12;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 11
US-09-187-330-3
; Sequence 3, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana

; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; OTHER INFORMATION: (ADNF III) cDNA clone
US-09-187-330-3

SEQ ID NO 3
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse activity dependent neurotrophic factor III

Qy   41 NAPVSIPQ 48
          ||||||||
Db   52 NAPVSIPQ 59

Query Match   33.9%;   Score 41;   DB 4;   Length 806;
Best Local Similarity   100.0%;   Pred. No. 12;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 12
US-09-187-330-55
; Sequence 55, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
US-09-187-330-55

SEQ ID NO 55
; LENGTH: 828
; TYPE: PRT
; ORGANISM: Mus musculus

Qy   41 NAPVSIPQ 48
          ||||||||
Db   74 NAPVSIPQ 81

Query Match   33.9%;   Score 41;   DB 4;   Length 828;
Best Local Similarity   100.0%;   Pred. No. 12;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 13
US-09-187-330-59

Sequence 59, Application US/09187330
Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 59
; LENGTH: 874
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-187-330-59

Query Match   33.9%;   Score 41; DB 4; Length 874;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   41 NAPVSIPQ 48
          |||||||||
Db   126 NAPVSIPQ 133

RESULT 14
US-09-187-330-1
Sequence 1, Application US/09187330
Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 1
; LENGTH: 1000
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: H3' human activity dependent neurotrophic factor
; FEATURE:
; OTHER INFORMATION: III (ADNF III) clone
; NAME/KEY: MOD_RES
; LOCATION: (801)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (817)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:

; NAME/KEY: MOD_RES
; LOCATION: (821)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (833)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (854)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (866)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (870)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (877)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (882)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (922)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (948)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (959)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (964)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (967)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (980)
; OTHER INFORMATION: Xaa = unknown
US-09-187-330-1

Query Match   33.9%;   Score 41; DB 4; Length 1000;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   41 NAPVSIPQ 48
          |||||||||
Db   52 NAPVSIPQ 59

RESULT 15
US-09-364-609-8
Sequence 8, Application US/09364609A
Patent No. 6649411
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Zamostiano, Rachel
; APPLICANT: Gelber, Edgar
; APPLICANT: Pinhasov, Albert
; APPLICANT: Bassan, Merav

```
; APPLICANT: Ramot University Authority for Applied Research &
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Methods of Inhibiting Cancer Cells with ADNF III
; TITLE OF INVENTION: Antisense Oligonucleotides
; FILE REFERENCE: 019856-00010US
; CURRENT APPLICATION NUMBER: US/09/364,609A
; CURRENT FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 8
; LENGTH: 1102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human activity dependent neurotrophic factor III
; OTHER INFORMATION: (ADNF III) cDNA
US-09-364-609-8
```

```
Query Match          33.9%;  Score 41;  DB 4;  Length 1102;
Best Local Similarity 100.0%;  Pred. No. 16;
Matches    8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    41 NAPVSIPQ 48
         ||||||||
Db   354 NAPVSIPQ 361
```

Search completed: February 23, 2005, 19:36:17
Job time : 38.8305 secs

OM protein - protein search, using sw model

Run on: February 23, 2005, 19:34:28 ; Search time 88 Seconds
(without alignments)
327.241 Million cell updates/sec

GenCore version 5.1.6
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Title: US-09-267-511-4
Perfect Score: 121
Sequence: 1 XXXXXXXXXXXXXXXXXX.........XXXXXXXXXXXXXXXXXXX 88

Scoring table: BLOSUM62
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Searched: 1380268 seqs, 327241040 residues
Total number of hits satisfying chosen parameters: 1380268

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
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Database :
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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	41	33.9	8	9	US-09-267-511-2	Sequence 2, Appli
2	41	33.9	14	15	US-10-164-432-4	Sequence 4, Appli
3	41	33.9	8	15	US-10-296-849-2	Sequence 2, Appli
4	41	33.9	8	15	US-10-623-272-6	Sequence 6, Appli
5	41	33.9	10	9	US-09-267-511-23	Sequence 23, Appl
6	41	33.9	10	15	US-10-296-849-20	Sequence 20, Appl
7	41	33.9	10	15	US-10-623-272-33	Sequence 33, Appl
8	41	33.9	13	15	US-10-623-272-24	Sequence 24, Appl
9	41	33.9	13	15	US-10-296-849-21	Sequence 21, Appl
10	41	33.9	15	15	US-10-623-272-34	Sequence 34, Appl
11	41	33.9	9	15	US-09-267-511-25	Sequence 25, Appl
12	41	33.9	15	15	US-10-296-849-22	Sequence 22, Appl
13	41	33.9	15	15	US-10-623-272-35	Sequence 35, Appl
14	41	33.9	17	9	US-09-267-511-19	Sequence 19, Appl
15	41	33.9	17	9	US-09-267-511-26	Sequence 26, Appl
16	41	33.9	9	9	US-09-267-511-18	Sequence 18, Appl
17	41	33.9	9	9	US-09-267-511-20	Sequence 20, Appl
18	41	33.9	18	15	US-10-296-849-23	Sequence 23, Appl
19	41	33.9	18	15	US-10-623-272-12	Sequence 12, Appl
20	41	33.9	8	9	US-09-267-511-4	Sequence 4, Appli
21	41	33.9	18	15	US-10-296-849-13	Sequence 13, Appl
22	41	33.9	88	15	US-10-623-272-10	Sequence 10, Appl
23	41	33.9	88	15	US-10-623-272-57	Sequence 57, Appl
24	41	33.9	726	15	US-10-623-272-32	Sequence 32, Appl
25	41	33.9	781	15	US-10-623-272-31	Sequence 31, Appl
26	41	33.9	787	15	US-10-623-272-41	Sequence 41, Appl
27	41	33.9	800	15	US-10-623-272-3	Sequence 3, Appli
28	41	33.9	806	15	US-10-623-272-55	Sequence 55, Appl
29	41	33.9	828	15	US-10-623-272-59	Sequence 59, Appl
30	41	33.9	874	15	US-10-623-272-1	Sequence 1, Appli
31	41	33.9	1000	15	US-10-623-272-2	Sequence 2, Appli
32	41	33.9	1102	14	US-09-364-609-8	Sequence 8, Appl
33	41	33.9	1102	15	US-11-164-432-2	Sequence 2, Appl
34	36	29.8	1102	15	US-10-221-625-49	Sequence 49, Appl
35	36	29.8	1102	15	US-10-623-272-28	Sequence 28, Appl
36	36	29.8	9	15	US-10-169-048-18	Sequence 18, Appl
37	36	29.8	510	15	US-10-264-213-145	Sequence 145, App
38	36	29.8	510	15	US-10-282-122A-42533	Sequence 42533, A
39	36	29.8	511	15	US-10-282-122A-74577	Sequence 74577, A
40	35	28.9	321	15	US-10-282-122A-72068	Sequence 72068, A
41	35	28.9	511	15	US-10-425-114-58854	Sequence 58854, A
42	35	28.9	808	16	US-10-282-122A-61671	Sequence 61671, A
43	34	28.1	103	16	US-10-437-963-141033	Sequence 141033, A
44	34	28.1	503	15	US-10-424-599-178130	Sequence 178130,
45	33	27.3	78	14	US-10-029-386-32792	Sequence 32792, A

ALIGNMENTS

RESULT 1
US-09-267-511-2

; Sequence 2, Application US/09267511
; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death with ADNF Polypeptides
; FILE REFERENCE: 015280-3770000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:activity
; OTHER INFORMATION: dependent neurotrophic factor III (ADNF III)
; OTHER INFORMATION: active site
US-09-267-511-2

Query Match   33.9%; Score 41; DB 9; Length 8;
Best Local Similarity   100.0%; Pred. No. 1.2e+06;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
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Db   1 NAPVSIPQ 8

RESULT 2
US-10-164-432-4
Sequence 4, Application US/10164432
Publication No. US20030166544A1
GENERAL INFORMATION:
APPLICANT: Alcon Inc.
APPLICANT: Clark, Abbot F.
APPLICANT: Debra, Shade L.
CURRENT APPLICATION NUMBER: US/10/164,432
CURRENT FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: 09/921,029
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/230,964
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 8
TYPE: PRT
ORGANISM: homo sapiens
TITLE OF INVENTION: The Use of ADNP for the Treatment of Glaucomatous Optic Neuropath
FILE REFERENCE: 1975A US
US-10-164-432-4

Query Match   33.9%;   Score 41;   DB 14;   Length 8;
Best Local Similarity   100.0%;   Pred. No. 1.2e+06;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 3
US-10-296-849-2
Sequence 2, Application US/10296849
Publication No. US20040048801A1
GENERAL INFORMATION:
APPLICANT: Spong, Catherine Y.
APPLICANT: Brenneman, Douglas
APPLICANT: Gozes, Illana
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied and
APPLICANT: Industrial Development, Ltd.
TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
FILE REFERENCE: 15200W-0042000US
CURRENT APPLICATION NUMBER: US/10/296,849
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/208,944
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: US 60/267,805
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: WO PCT/US01/17758
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Activity
OTHER INFORMATION: Dependent Neurotrophic Factor III (ADNF III)
OTHER INFORMATION: active core site, NAP or ADNF III-8
US-10-296-849-2

Qy   41 NAPVSIPQ 48
         |||||||||
Db   1 NAPVSIPQ 8

Query Match   33.9%;   Score 41;   DB 15;   Length 8;
Best Local Similarity   100.0%;   Pred. No. 1.2e+06;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 4
US-10-623-272-6
Sequence 6, Application US/10623272
Publication No. US20040053313A1
GENERAL INFORMATION:
APPLICANT: Gozes, Illana
APPLICANT: Brenneman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamostiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-2912000US
CURRENT APPLICATION NUMBER: US/10/623,272
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III-8
OTHER INFORMATION: active site core peptide, clone 25 sequence (NAP)
US-10-623-272-6

Qy   41 NAPVSIPQ 48
         |||||||||
Db   1 NAPVSIPQ 8

Query Match   33.9%;   Score 41;   DB 15;   Length 8;
Best Local Similarity   100.0%;   Pred. No. 1.2e+06;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 5
US-09-267-511-23
Sequence 23, Application US/09267511
Patent No. US20020111301A1
GENERAL INFORMATION:
APPLICANT: Brenneman, Douglas E.
APPLICANT: Spong, Catherine Y.
APPLICANT: Gozes, Illana
APPLICANT: Bassan, Merav
APPLICANT: Zamostiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied Research
APPLICANT: and Industrial Development, Ltd.
TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
TITLE OF INVENTION: Death With ADNF Polypeptides
FILE REFERENCE: 012280-37700US
CURRENT APPLICATION NUMBER: US/09/267,511
CURRENT FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-267-511-23

Qy    41 NAPVSIPQ 48
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Db     3 NAPVSIPQ 10

Query Match    33.9%;  Score 41;  DB 9;  Length 10;
Best Local Similarity   100.0%;  Pred. No. 0.33;
Matches  8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 6
US-10-296-849-20
; Sequence 20, Application US/10296849
; Publication No. US20040048801A1
; GENERAL INFORMATION:
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Brenneman, Douglas
; APPLICANT: Gozes, Illana
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied and
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
; FILE REFERENCE: 15280W-004200US
; CURRENT APPLICATION NUMBER: US/10/296,849
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/208,944
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 60/267,805
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: WO PCT/US01/17758
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-10-296-849-20

Qy    41 NAPVSIPQ 48
         ||||||||
Db     3 NAPVSIPQ 10

Query Match    33.9%;  Score 41;  DB 15;  Length 10;
Best Local Similarity   100.0%;  Pred. No. 0.33;
Matches  8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 7
US-10-623-272-33
; Sequence 33, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 33
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-10-623-272-33

Qy    41 NAPVSIPQ 48
         ||||||||
Db     3 NAPVSIPQ 10

Query Match    33.9%;  Score 41;  DB 15;  Length 10;
Best Local Similarity   100.0%;  Pred. No. 0.33;
Matches  8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 8
US-09-267-511-24
; Sequence 24, Application US/09267511
; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-267-511-24

Qy    41 NAPVSIPQ 48
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Db     4 NAPVSIPQ 11

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Best Local Similarity   100.0%;  Pred. No. 0.44;
Matches  8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 9
US-10-296-849-21
; Sequence 21, Application US/10296849
```

Publication No. US20040048801A1
GENERAL INFORMATION:
APPLICANT: Spong, Catherine Y.
APPLICANT: Brenneman, Douglas
APPLICANT: Gozes, Illana
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied and
APPLICANT: Industrial Development, Ltd.
TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
FILE REFERENCE: 15280W-0042000US
CURRENT APPLICATION NUMBER: US/10/296,849
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/208,944
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: US 60/267,805
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: WO PCT/US01/17758
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III
OTHER INFORMATION: polypeptide
US-10-296-849-21

Query Match   33.9%;   Score 41; DB 15; Length 13;
Best Local Similarity   100.0%; Pred. No. 0.44;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
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Db   4   NAPVSIPQ 11

RESULT 10
US-10-623-272-34
Sequence 34, Application US/10623272
Publication No. US20040053313A1
GENERAL INFORMATION:
APPLICANT: Gozes, Illana
APPLICANT: Brenneman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamostiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-291200US
CURRENT APPLICATION NUMBER: US/10/623,272
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III
US-10-623-272-34

Query Match   33.9%;   Score 41; DB 15; Length 13;
Best Local Similarity   100.0%; Pred. No. 0.44;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
          ||||||||
Db   4   NAPVSIPQ 11

RESULT 11
US-09-267-511-25
Sequence 25, Application US/09267511
Patent No. US20020113301A1
GENERAL INFORMATION:
APPLICANT: Brenneman, Douglas E.
APPLICANT: Spong, Catherine Y.
APPLICANT: Gozes, Illana
APPLICANT: Bassan, Merav
APPLICANT: Zamostiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied Research
APPLICANT: and Industrial Development, Ltd.
TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
TITLE OF INVENTION: Death With ADNF Polypeptides
FILE REFERENCE: 015280-377000US
CURRENT APPLICATION NUMBER: US/09/267,511
CURRENT FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III
OTHER INFORMATION: polypeptide
US-09-267-511-25

Query Match   33.9%;   Score 41; DB 9; Length 15;
Best Local Similarity   100.0%; Pred. No. 0.52;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
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Db   6   NAPVSIPQ 13

RESULT 12
US-10-296-849-22
Sequence 22, Application US/10296849
Publication No. US20040048801A1
GENERAL INFORMATION:
APPLICANT: Spong, Catherine Y.
APPLICANT: Brenneman, Douglas
APPLICANT: Gozes, Illana
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied and
APPLICANT: Industrial Development, Ltd.
TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
FILE REFERENCE: 15280W-0042000US
CURRENT APPLICATION NUMBER: US/10/296,849
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/208,944
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: US 60/267,805
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: WO PCT/US01/17758
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 23

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-10-296-849-22

Qy      41 NAPVSIPQ 48
           ||||||||
Db       6 NAPVSIPQ 13

Query Match      33.9%;   Score 41;  DB 15;  Length 15;
Best Local Similarity  100.0%;   Pred. No. 0.52;
Matches  8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 13
US-10-623-272-35
; Sequence 35, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
;           as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-29120US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-10-623-272-35

Qy      41 NAPVSIPQ 48
           ||||||||
Db       6 NAPVSIPQ 13

Query Match      33.9%;   Score 41;  DB 15;  Length 15;
Best Local Similarity  100.0%;   Pred. No. 0.52;
Matches  8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 14
US-09-267-511-19
; Sequence 19, Application US/09267511
; Patent No. US2002011301A1
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-37700000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-267-511-19

Qy      41 NAPVSIPQ 48
           ||||||||
Db       6 NAPVSIPQ 13

Query Match      33.9%;   Score 41;  DB 9;  Length 17;
Best Local Similarity  100.0%;   Pred. No. 0.59;
Matches  8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 15
US-09-267-511-26
; Sequence 26, Application US/09267511
; Patent No. US2002011301A1
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-37700000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-267-511-26

Qy      41 NAPVSIPQ 48
           ||||||||
Db       8 NAPVSIPQ 15

Query Match      33.9%;   Score 41;  DB 9;  Length 17;
Best Local Similarity  100.0%;   Pred. No. 0.59;
Matches  8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


Search completed: February 23, 2005, 19:51:27
Job time : 88 secs
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us-09-267-511-4.rapb

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OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: February 23, 2005, 19:09:56 ; Search time 114.35 Seconds
(without alignments)
394.078 Million cell updates/sec

Title: US-09-267-511-4
Perfect score: 121
Sequence: 1 XXXXXXXXXXXXXXXXXXX...............XXXXXXXXXXXXXXXXXXXX 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	41	33.9	823	1	Q9jk18	ADNP_RAT	rattus norv
2	41	33.9	828	1	Q9z103	ADNP_MOUSE	mus musculu
3	41	33.9	1089	2	Q6zq47		mus musculu
4	41	33.9	1102	1	Q9h2p0	ADNP_HUMAN	homo sapien
5	41	33.9	1102	1	Q6dhz8		homo sapien
6	36	29.8	445	2	Q6c9b5		yarrowia li
7	36	29.8	470	2	Q82yw3		enterococcu
8	36	29.8	481	2	Q8e338		streptococc
9	36	29.8	510	2	Q8p023		streptococc
10	36	29.8	510	2	Q99zk7		streptococc
11	36	29.8	510	2	Q8k7f1		streptococc
12	36	29.8	511	2	Q8duc1		streptococc
13	36	29.8	631	2	Q9i2g3		pseudomonas
14	36	29.8	1396	2	Q8bx17		mus musculu
15	36	29.8	1502	1	GEM5_MOUSE		mus musculu
16	35	29.8	189	2	Q8szd3		drosophila
17	35	29.8	189	2	Q9v728		drosophila
18	35	28.9	299	2	Q92xp0		rhizobium m
19	35	28.9	3415	2	Q9xcf3		mycobacteri
20	35	28.9	4027	2	Q740v0		mycobacteri
21	34	28.9	136	2	O28744		archaeoglob
22	34	28.1	158	2	O8bqb7		mus musculu
23	34	28.1	464	2	O6ffk0		mus musculu
24	34	28.1	503	2	Q84lk3		oryza sativ
25	34	28.1	505	2	Q9v3b2		acinetobact
26	34	28.1	597	2	Q6maf9		drosophila
27	34	28.1	1272	1	FMR2_MOUSE		mus musculu
28	34	28.1	1272	1	FMR2_PANTR		pan troglod
29	34	28.1	1272	1	FMR2_PONPY		pongo pygma
30	34	28.1	1272	2	Q7z400		homo sapien
31	34	28.1	1311	1	FMR2_HUMAN		homo sapien
32	34	28.1	1789	2	Q8t145	Q8t145	dictyosteli
33	33	27.3	104	2	Q8a044	Q8a044	bacteroides
34	33	27.3	197	1	Q8z7n9	WRBA_SALTI	salmonella
35	33	27.3	197	1	Q8zq40	WRBA_SALTY	salmonella
36	33	27.3	231	1	Q7vj02	HIS2_HELHP	helicobacte
37	33	27.3	253	2	Q6w4c2	Q6w4c2	drosophila
38	33	27.3	253	2	Q6w4c3	Q6w4c3	drosophila
39	33	27.3	258	2	Q6w4e3	Q6w4e3	drosophila
40	33	27.3	253	2	Q6c7g0	Q6c7g0	yarrowia li
41	33	27.3	350	2	Q6fex1	Q6fex1	acinetobact
42	33	27.3	418	2	O02468	O02468	drosophila
43	33	27.3	467	2	Q9zfv2	EUTA_SALTY	salmonella
44	33	27.3	467	2	Q8z4u1	EUTA_SALTI	salmonella
45	33	27.3	468	2	Q6lw58	Q6lw58	photobacter

ALIGNMENTS

RESULT 1
ADNP_RAT
ID   ADNP_RAT   STANDARD;   PRT;   823 AA.
AC   Q9JK18;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Activity-dependent neuroprotector (Activity-dependent neuroprotective
DE   protein).
GN   Name=Adnp;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dong M., Xu K., Du Y.;
RT   "Complete sequence of a rat protein containing a femtomolar-activity-
RT   dependent neuroprotective peptide.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Potential transcription factor. May mediate some of the
CC   neuroprotective peptide VIP-associated effects involving normal
CC   growth and cancer proliferation.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- INDUCTION: By the neuroprotective peptide VIP.
CC   -!- SIMILARITY: Contains 1 homeobox domain.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; AF234680; AAF40431.1; -.
DR   RGD; 71030; Adnp.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR001356; Homeodomain_like.
DR   InterPro; IPR009057; Homeodomain_like.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF00046; Homeobox; 1.
DR   Pfam; PF00096; zf-C2H2; 1.
DR   SMART; SM00389; HOX; 1.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW   DNA-binding; Homeobox; Metal-binding; Nuclear protein; Repeat;
KW   Transcription regulation; Zinc-finger.
FT   ZN_FING   167   189   C2H2-type 1 (atypical).
FT   ZN_FING   209   230   C2H2-type 2.
FT   ZN_FING   232   255   C2H2-type 3.
FT   ZN_FING   342   367   C2H2-type 4 (atypical).

FT   ZN FING   382   406   C2H2-type 5 (atypical).
FT   DNA BIND   474   534   Homeobox.
SQ   SEQUENCE 823 AA; 91335 MW; A4C4BC616052BDBF CRC64;

Qy   41 NAPVSIPQ 48
        ||||||||
Db   74 NAPVSIPQ 81

Query Match   33.9%; Score 41; DB 1; Length 823;
Best Local Similarity 100.0%; Pred. No. 13;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 2
ID   ADNP_MOUSE   STANDARD;   PRT;   828 AA.
AC   Q9Z103;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Activity-dependent neuroprotector (Activity-dependent neuroprotective
DE   protein).
GN   Name=Adnp;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND SYNTHESIS OF 74-81.
RC   TISSUE=Brain;
RX   MEDLINE=99155106; PubMed=10037502;
RA   Bassan M., Zamostiano R., Davidson A., Pinhasov A., Giladi E.,
RA   Perl O., Bassan H., Blat C., Gibney G., Glazner G., Brenneman D.E.,
RA   Gozes I.;
RT   "Complete sequence of a novel protein containing a femtomolar-
RT   activity-dependent neuroprotective peptide.";
RL   J. Neurochem. 72:1283-1293(1999).
CC   -!- FUNCTION: Potential transcription factor. May mediate some of the
CC   neuroprotective peptide VIP-associated effects involving normal
CC   growth and cancer proliferation.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- TISSUE SPECIFICITY: Expressed in the brain, with a higher
CC   expression in cerebellum and hippocampus. Weakly expressed in
CC   lung, kidney and intestine, and expressed at intermediate level in
CC   testis.
CC   -!- INDUCTION: By the neuroprotective peptide VIP.
CC   -!- MISCELLANEOUS: When isolated from the sequence, the
CC   neuroprotective peptide provides neuroprotection at subfemtomolar
CC   concentrations against toxicity associated with tetrodoxin
CC   (electrical blockade), the beta-amyloid peptide (the Alzheimer's
CC   disease neurotoxin), N-methyl-aspartate (excitotoxicity), and the
CC   human immunodeficiency virus (HIV) envelope protein.
CC   -!- SIMILARITY: Contains 1 homeobox domain.

DR   EMBL; AF061198; AAD19843.1; -.
DR   MGD; MGI:1338758; Adnp.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR009057; Homeodomain_like.
DR   InterPro; IPR007087; ZnF_C2H2.
DR   Pfam; PF00046; Homeobox_1.
DR   Pfam; PF00096; zf-C2H2; 1.
DR   SMART; SM00389; HOX; 1.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW   DNA-binding; Homeobox; Metal-binding; Nuclear protein; Repeat;
KW   Transcription regulation; Zinc-finger.
FT   ZN FING   166   188   C2H2-type 1 (atypical).
FT   ZN FING   208   229   C2H2-type 2.
FT   ZN FING   231   254   C2H2-type 3.
FT   ZN FING   341   366   C2H2-type 4 (atypical).
FT   ZN FING   381   405   C2H2-type 5 (atypical).
FT   DNA BIND   473   533   Homeobox.
FT   SITE   74   81   Neuroprotective peptide.
FT   DOMAIN   599   670   Glu-rich.
SQ   SEQUENCE 828 AA; 92063 MW; 9DF66695C506EB8606 CRC64;

Qy   41 NAPVSIPQ 48
        ||||||||
Db   74 NAPVSIPQ 81

Query Match   33.9%; Score 41; DB 1; Length 828;
Best Local Similarity 100.0%; Pred. No. 13;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 3
ID   Q6ZQ47   PRELIMINARY;   PRT;   1089 AA.
AC   Q6ZQ47;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MKIAA0784 protein (Fragment).
GN   Name=mKIAA0784;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=14621295;
RA   Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA   Saga Y., Nagase T., Ohara O., Koga H.;
RT   "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT   III. the complete nucleotide sequences of 500 mouse homologues of KIAA-homologous
RT   cDNAs identified by screening of terminal sequences of cDNA clones
RT   randomly sampled from size-fractionated libraries.";
RL   DNA Res. 10:167-180(2003).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR   EMBL; AK129214; BAC98024.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR007087; ZnF_C2H2.
DR   Pfam; PF00046; Homeobox_1.
DR   Pfam; PF00096; zf-C2H2; 1.
DR   SMART; SM00389; HOX; 1.
DR   SMART; SM00355; ZnF_C2H2; 8.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW   DNA-binding; Homeobox; Nuclear protein.
NON_TER   1   1
SQ   SEQUENCE 1089 AA; 122152 MW; 7FF389C7FABDF660 CRC64;

Query Match   33.9%; Score 41; DB 2; Length 1089;
Best Local Similarity 100.0%; Pred. No. 17;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
        ||||||||
Db   335 NAPVSIPQ 342

RESULT 4

ID   ADNP_HUMAN   STANDARD;   PRT;   1102 AA.
AC   Q9H2P0; Q94881; Q9UG34;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Activity-dependent neuroprotector (Activity-dependent neuroprotective
DE   protein).
GN   Name=ADNP; Synonyms=KIAA0784;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RX   PubMed=11013255; DOI=10.1074/jbc.M007416200;
RA   Zamostiano R., Pinhasov A., Gelber E., Steingart R.A., Seroussi E.,
RA   Giladi E., Bassan M., Wollman Y., Eyre H.J., Mulley J.C.,
RA   Brenneman D.E., Gozes I.;
RT   "Cloning and characterization of the human activity-dependent
RT   neuroprotective protein.";
RL   J. Biol. Chem. 276:708-714(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA   Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [3]
RP   SEQUENCE OF 30-1102 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=99087487; PubMed=9872452;
RA   Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
RA   Tanaka A., Kotani H., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XI.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 5:277-286(1998).
RN   [4]
RP   SEQUENCE OF 98-1102 FROM N.A.
RC   TISSUE=Uterus;
RA   Wambutt R., Heubner D., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Potential transcription factor. May mediate some of the
CC   neuroprotective peptide VIP-associated effects involving normal
CC   growth and cancer proliferation.

CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- TISSUE SPECIFICITY: Widely expressed. Strong expression in heart,
CC   skeletal muscle, kidney and placenta. In brain, expression is
CC   stronger in the cerebellum and cortex regions. No expression
CC   detected in the colon. Strong increase of expression in colon and
CC   breast cancer tissues.
CC   -!- SIMILARITY: Contains 1 homeobox domain.
CC   ---
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CC   ---
DR   EMBL; AF250860; AAG47651.1; -.
DR   EMBL; AL034553; CAB37748.2; -.
DR   EMBL; AB018327; BAA34504.1; -.
DR   EMBL; AL080163; CAB45752.1; -.
DR   PIR; T12546; T12546.
DR   Genew; HGNC:15766; ADNP.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR011356; Homeobox.
DR   InterPro; IPR009057; Homeodomain_like.
DR   InterPro; IPR007087; ZnF_C2H2.
DR   Pfam; PF00046; Homeobox; 1.
DR   Pfam; PF00096; zf-C2H2; 2.
DR   SMART; SM00389; HOX; 1.
DR   SMART; SM00355; ZnF_C2H2; 8.
DR   PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW   Transcription regulation; Zinc-finger;
KW   DNA-binding; Homeobox; Metal-binding; Nuclear protein; Repeat;
FT   ZN_FING   74   97   C2H2-type 1.
FT   ZN_FING   107   129   C2H2-type 2 (atypical).
FT   ZN_FING   165   188   C2H2-type 3.
FT   ZN_FING   221   244   C2H2-type 4.
FT   ZN_FING   447   469   C2H2-type 5 (atypical).
FT   ZN_FING   489   510   C2H2-type 6 (atypical).
FT   ZN_FING   512   535   C2H2-type 7.
FT   ZN_FING   622   647   C2H2-type 8 (atypical).
FT   ZN_FING   662   686   C2H2-type 9 (atypical).
FT   DNA_BIND   754   814   Homeobox.
SQ   SEQUENCE   1102 AA; 123562 MW; 4132E3EF814AF43B CRC64;

Qy   41 NAPVSIPQ 48
              ||||||||
Db   354 NAPVSIPQ 361

Query Match   33.9%; Score 41; DB 1; Length 1102;
Best Local Similarity   100.0%;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
              ||||||||
Db   354 NAPVSIPQ 361

RESULT 5

ID   Q6DH28   PRELIMINARY;   PRT;   1102 AA.
AC   Q6DH28;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Activity-dependent neuroprotector.
GN   Name=ADNP;
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; BC075794; AAH75794.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003439; Homeobox.
DR InterPro; IPR001356; Homeodomain_like.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00046; Homeobox; 1.
DR Pfam; PF00096; zf-C2H2; 1.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00355; ZnF_C2H2; 8.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
DR PROSITE; PS50211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
DR PROSITE; PS01157; ZINC_FINGER_C2H2_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 1102 AA; 123446 MW; 2B69848540C766A CRC64;

Query Match   33.9%; Score 41; DB 2; Length 1102;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   41 NAPVSIPQ 48
            ||||||||
Db   354 NAPVSIPQ 361

RESULT 6
ID   Q6C9B5
AC   Q6C9B5;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Similar to DEHA0D16797g Debaryomyces hansenii.
GN   ORFNames=YALI0D12496g;
OS   Yarrowia lipolytica CLIB99.
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Dipodascaceae; Yarrowia.
OX   NCBI_TaxID=284591;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CLIB99;
RG   GenoLevures;
RA   Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA   Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA   Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA   Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA   Boisramé A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA   Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA   Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA   Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA   Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA   Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA   Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA   Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA   Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA   Wincker P., Souciet J.L.;
RL   "Genome evolution in yeasts.";
RL   Nature 430:35-44(2004).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CLIB99;
RG   Genoscope;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR382130; CAG80935.1; -.
SQ   SEQUENCE 445 AA; 50191 MW; DB0039F405D2D9BBC CRC64;

Query Match   29.8%; Score 36; DB 2; Length 445;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy   41 NAPVSIPQ 48
            |:||||
Db   310 NTPISIPQ 317

RESULT 7
ID   Q82YW3
AC   Q82YW3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Citrate lyase, alpha subunit.
GN   Name=citF; OrderedLocusNames=EF3319;
OS   Enterococcus faecalis (Streptococcus faecalis).
OC   Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX   NCBI_TaxID=1351;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=V583 / ATCC 700802;
RX   MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA   Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA   Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA   Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA   Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA   Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA   Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA   Fraser C.M.;
RT   "Role of mobile DNA in the evolution of vancomycin-resistant
RT   Enterococcus faecalis.";
RL   Science 299:2071-2074(2003).
DR   EMBL; AE016957; AAO82984.1; -.
DR   TIGR; EF3319; -.
DR   GO; GO:0009346; C:citrate lyase complex; IEA.
DR   GO; GO:0008814; F:citrate CoA-transferase activity; IEA.
DR   GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
DR   InterPro; IPR006472; CitF.
DR   Pfam; PF04223; CitF; 1.
DR   PIRSF; PIRSF009451; Citrt_lyas_alpha; 1.
DR   TIGRFAMs; TIGR01584; cirF; 1.
KW   Complete proteome.
SQ   SEQUENCE 470 AA; 50138 MW; 80B31677443C93 CRC64;

Query Match   29.8%; Score 36; DB 2; Length 470;
Best Local Similarity 75.0%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy   41 NAPVSIPQ 48
        |:|:|||
Db  175 NTPISIPQ 182

RESULT 8
Q8E338
ID   Q8E338;             PRELIMINARY;      PRT;   481 AA.
AC   Q8E338;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein gbs1925.
GN   OrderedLocusNames=gbs1925;
OS   Streptococcus agalactiae (serotype III).
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=216495;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NEM316 / Serotype III;
RX   MEDLINE=22242508; PubMed=12354221;
RA   Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
RA   Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA   Kunst F.;
RT   "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT   invasive neonatal disease.";
RL   Mol. Microbiol. 45:1499-1513(2002).
DR   EMBL; AL766854; CAD47584.1; -.
DR   Sagalist; gbs1925; -.
DR   InterPro; IPR006270; Strep_his_triad.
DR   Pfam; PF04270; Strep_his_triad; 4.
DR   TIGRFAMs; TIGR01363; strep_his_triad; 1.
KW   Complete proteome.
SQ   SEQUENCE  481 AA;  53326 MW;  DFDF0453D8A929BE CRC64;

Query Match          29.8%;  Score 36;  DB 2;  Length 481;
Best Local Similarity   75.0%;  Pred. No. 79;
Matches    6;  Conservative   2;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   41 NAPVSIPQ 48
        |||:|||:
Db  281 NAPISIPR 288
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RESULT 9
Q8P0Z3
ID   Q8P0Z3;             PRELIMINARY;      PRT;   510 AA.
AC   Q8P0Z3;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative citrate lyase, alpha subunit.
GN   Name=citF; OrderedLocusNames=spyM18_1140;
OS   Streptococcus pyogenes (serotype M18).
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=186103;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MGAS8232;
RX   MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.06252609;
RA   Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA   Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA   Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA   Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT   "Genome sequence and comparative microarray analysis of serotype M18
RT   group A Streptococcus strains associated with acute rheumatic fever
RT   outbreaks.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
DR   EMBL; AE010039; AAL97760.1; -.
DR   GO; GO:0009346; C:citrate lyase complex; IEA.
DR   GO; GO:0008814; F:citrate CoA-transferase activity; IEA.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0016829; F:lyase activity; IEA.
DR   ProDom; PD003528; ETF_beta; 1.
DR   GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006472; CitF.
DR   InterPro; IPR000049; ETF_beta.
DR   Pfam; PF04223; CitF; 1.
DR   PIRSF; PIRSF009451; Citrt_lyas_alpha; 1.
DR   TIGRFAMs; TIGR01584; CitF; 1.
KW   Complete proteome; Lyase.
SQ   SEQUENCE  510 AA;  54918 MW;  05F3E30FD0BAD4DF CRC64;

Query Match          29.8%;  Score 36;  DB 2;  Length 510;
Best Local Similarity   75.0%;  Pred. No. 84;
Matches    6;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy   41 NAPVSIPQ 48
        |:|:||||
Db  215 NTPISIPQ 222
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RESULT 10
Q99ZK7
ID   Q99ZK7;             PRELIMINARY;      PRT;   510 AA.
AC   Q99ZK7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative citrate lyase, alpha subunit (EC 4.1.3.6).
GN   Name=citF; OrderedLocusNames=SPy1189;
OS   Streptococcus pyogenes.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1314;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX   MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
RA   Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA   Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA   Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
RA   Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
RT   "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR   EMBL; AE006559; AAK34053.1; -.
DR   GO; GO:0009346; C:citrate lyase complex; IEA.
DR   GO; GO:0008815; C:citrate (pro-3S)-lyase activity; IEA.
DR   GO; GO:0008814; F:citrate CoA-transferase activity; IEA.
DR   GO; GO:0016829; F:lyase activity; IEA.
DR   GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
DR   InterPro; IPR006472; CitF.
DR   Pfam; PF04223; CitF; 1.
DR   PIRSF; PIRSF009451; Citrt_lyas_alpha; 1.
DR   TIGRFAMs; TIGR01584; CitF; 1.
KW   Complete proteome; Lyase.
SQ   SEQUENCE  510 AA;  54990 MW;  459833B693E2EFA7 CRC64;

Query Match          29.8%;  Score 36;  DB 2;  Length 510;
Best Local Similarity   75.0%;  Pred. No. 84;
Matches    6;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy   41 NAPVSIPQ 48
        |:|:||||
Db  215 NTPISIPQ 222
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RESULT 11
Q8K7F1
ID   Q8K7F1;             PRELIMINARY;      PRT;   510 AA.
AC   Q8K7F1; Q79X56;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
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DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative citrate lyase, alpha subunit.
GN   Name=citF; OrderedLocusNames=SPs1034; SpyM3_0834;
OS   Streptococcus pyogenes (serotype M3).
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=198466;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MGAS315 / Serotype M3;
RX   MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA   Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
RA   Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA   Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA   Schlievert P.M., Musser J.M.;
RT   "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT   phage-encoded toxins, the high-virulence phenotype, and clone
RT   emergence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN-SSI-1;
RX   MEDLINE=22683278; PubMed=1279345; DOI=10.1101/gr.1096703;
RA   Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA   Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA   Hayashi H., Hattori M., Hamada S.;
RT   "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT   large-scale genomic rearrangement in invasive strains and new insights
RT   into phage evolution.";
RL   Genome Res. 13:1042-1055(2003).
DR   EMBL; AE014153; AAM79441.1; -.
DR   EMBL; AP005144; BAC64129.1; -.
DR   GO; GO:0009346; C:citrate lyase complex; IEA.
DR   GO; GO:0008815; F:citrate (pro-3S)-lyase activity; IEA.
DR   GO; GO:0008814; F:citrate CoA-transferase activity; IEA.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0016829; F:lyase activity; IEA.
DR   GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006472; CitF.
DR   InterPro; IPR000049; ETF_beta.
DR   Pfam; PF04223; CitF; 1.
DR   PIRSF; PIRSF009451; Citrt_lyas_alpha; 1.
DR   ProDom; PD003528; ETF_beta; 1.
DR   TIGRFAMs; TIGR01584; CitF; 1.
KW   Lyase; Complete proteome.
SQ   SEQUENCE 510 AA; 54890 MW; F84036E9F2B0D9A8 CRC64;

Query Match   29.8%; Score 36; DB 2; Length 510;
Best Local Similarity   75.0%; Pred. No. 84;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
                |:|:||||
Db   215 NTPISIPQ 222

Query Match   29.8%; Score 36; DB 2; Length 511;
Best Local Similarity   75.0%; Pred. No. 84;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
                |:|:||||
Db   215 NTPISIPQ 222

RESULT 12
ID   Q8DUC1   PRELIMINARY;   PRT;   511 AA.
AC   Q8DUC1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2004 (TrEMBLrel. 25, Last annotation update)
DE   Putative citrate lyase, alfa subunit (EC 4.1.3.6).
GN   Name=cilA; OrderedLocusNames=SMU.1021;
OS   Streptococcus mutans.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1309;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=UA159 / ATCC 700610 / Serotype c;

RX   MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
RA   Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA   Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA   Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
RA   Ferretti J.J.;
RT   "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT   pathogen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
DR   EMBL; AE014941; AAN58721.1; -.
DR   GO; GO:0009346; C:citrate lyase complex; IEA.
DR   GO; GO:0008815; F:citrate (pro-3S)-lyase activity; IEA.
DR   GO; GO:0008814; F:citrate CoA-transferase activity; IEA.
DR   GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
DR   InterPro; IPR006472; CitF.
DR   Pfam; PF04223; CitF; 1.
DR   PIRSF; PIRSF009451; Citrt_lyas_alpha; 1.
DR   TIGRFAMs; TIGR01584; citF; 1.
KW   Complete proteome.
SQ   SEQUENCE 511 AA; 55455 MW; FP966EB258334174 CRC64;

Query Match   29.8%; Score 36; DB 2; Length 511;
Best Local Similarity   75.0%; Pred. No. 84;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
                |:|:||||
Db   215 NTPISIPQ 222

RESULT 13
ID   Q912G3   PRELIMINARY;   PRT;   631 AA.
AC   Q912G3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=PA1941;
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
DR   EMBL; AE004620; AAG05329.1; -.
DR   PIR; B83404; B83404.
DR   InterPro; IPR003345; CytC_heme_BS.
DR   InterPro; IPR009056; Cytochrome_c.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE 631 AA; 70904 MW; E72A4692AEEB75F1 CRC64;

Query Match   29.8%; Score 36; DB 2; Length 631;
Best Local Similarity   87.5%; Pred. No. 1.1e+02;
Matches   7; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
                |||||:||
Db   263 NAPVSYPQ 270

RESULT 14

```
Q6KAS0
ID   Q6KAS0      PRELIMINARY;      PRT;  1396 AA.
AC   Q6KAS0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MFLJ00137 protein (Fragment).
GN   Name=mFLJ00137;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA   Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;
RT   "Prediction of the Coding Sequences of Mouse Homologues of FLJ Genes:
RT   The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous cDNAs
RT   Identified by Screening of Terminal Sequences of cDNA Clones Randomly
RT   Sampled from Size-Fractionated Libraries.";
RL   DNA Res. 11:167-180(2004).
CC   -!- SIMILARITY: Contains 9 WD repeats.
CC   -----------------------------------------------------------------------
DR   EMBL; AK131137; BAD21387.1; -.
DR   InterPro; IPR002114; HPr_SerP_S.
DR   InterPro; IPR001680; WD40.
DR   InterPro; IPR011046; WD40_like.
DR   Pfam; PF00400; WD40; 9.
DR   PRINTS; PR00320; GPROTEINBRPT.
DR   ProDom; PD000018; WD40; 11.
DR   SMART; SM00320; WD40; 11.
DR   PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
DR   PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_2.
DR   PROSITE; PS50082; WD_REPEATS_2; 2.
DR   PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW   Repeat; WD repeat.
FT   NON_TER       1       1
SQ   SEQUENCE   1396 AA;  155525 MW;  1E64S1D794FB06A0 CRC64;

Qy           41 NAPVSIPQ 48
                |||:||:|
Db         1314 NAPVSLPE 1321

Query Match             29.8%;
Best Local Similarity   75.0%;
Matches    6;  Conservative   2;  Mismatches   0;  Indels   0;  Gaps   0;

Score 36;  DB 2;  Length 1396;
```

```
RESULT 15
GEM5_MOUSE
ID   GEM5_MOUSE     STANDARD;      PRT;  1502 AA.
AC   Q8BXI7;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Gem-associated protein 5 (Gemin5).
GN   Name=Gemin5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
CC   -!- FUNCTION: The SMN complex plays an essential role in spliceosomal
CC       snRNP assembly in the cytoplasm and is required for pre-mRNA
CC       splicing in the nucleus.
CC   -!- SUBUNIT: Part of the core SMN complex that contains SMN1, SIP1,
CC       GEMIN2, GEMIN3, GEMIN4, GEMIN5, GEMIN6 and GEMIN7. Interacts
CC       directly with SMN1, SNRPB, SNRPD1, SNRPD2, SNRPD3 and SNRPE (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear, found both in the nucleoplasm and
CC       in nuclear bodies called gems (Gemini of Cajal bodies) that are
CC       often in proximity to Cajal (coiled) bodies. Also found in the
CC       cytoplasm (By similarity).
CC   -!- SIMILARITY: Contains 13 WD repeats.
CC   -----------------------------------------------------------------------
```

```
DR   EMBL; AK049216; BAC33614.1; -.
DR   MGD; MGI:2449311; Gemin5.
DR   InterPro; IPR011048; Cyt_cd1_haem_C.
DR   InterPro; IPR008941; TPR-like.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF00400; WD40; 11.
DR   PRINTS; PR00320; GPROTEINBRPT.
DR   ProDom; PD000018; WD40; 13.
DR   SMART; SM00320; WD40; 1.
DR   PROSITE; PS00678; WD_REPEATS_1; 3.
DR   PROSITE; PS50082; WD_REPEATS_2; 3.
DR   PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW   Coiled coil; mRNA processing; mRNA splicing; Nuclear protein; Repeat;
KW   Spliceosome; WD repeat.
FT   REPEAT       62     104       WD 1.
FT   REPEAT      107     148       WD 2.
FT   REPEAT      150     189       WD 3.
FT   REPEAT      193     264       WD 4.
FT   REPEAT      280     321       WD 5.
FT   REPEAT      333     374       WD 6.
FT   REPEAT      377     417       WD 7.
FT   REPEAT      424     464       WD 8.
FT   REPEAT      468     509       WD 9.
FT   REPEAT      533     573       WD 10.
FT   REPEAT      576     622       WD 11.
FT   REPEAT      637     677       WD 12.
FT   REPEAT      680     720       WD 13.
FT   DOMAIN      738     746       Poly-Lys.
FT   DOMAIN     1355    1382       Coiled coil (Potential).
SQ   SEQUENCE   1502 AA;  165562 MW;  46F98CCE70E2971 CRC64;
```

Query Match   29.8%; Score 36; DB 1; Length 1502;
Best Local Similarity   75.0%; Pred. No. 2.7e+02;
Matches   6; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
             |.|.||.|:|:
Db   1420 NAPVSLPE 1427

Search completed: February 23, 2005, 19:34:18
Job time : 116.35 secs

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: February 23, 2005, 19:22:32 ; Search time 24.3616 Seconds
(without alignments)
347.559 Million cell updates/sec

Title: US-09-267-511-4
Perfect score: 121
Sequence: 1 XXXXXXXXXXXXXXXXXXXX.........XXXXXXXXXXXXXXXXXXXX 88
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	41	33.9	1005	2	T12546	hypothetical prote
2	36	29.8	631	2	B83404	hypothetical prote
3	35	28.9	299	2	D95412	hypothetical prote
4	34	28.1	136	2	G69440	conserved hypothet
5	34	28.1	1272	2	T30248	fragile X mental r
6	33	27.3	198	2	A10632	trp repressor bind
7	33	27.3	467	2	AH0813	probable ethanolam
8	33	27.3	479	2	H86465	F12G12.1 protein -
9	33	27.3	601	2	S47896	probable molybdopt
10	33	27.3	1119	2	T50095	related to cytoske
11	33	27.3	1213	2	S16356	ovo protein - frui
12	33	27.3	2251	2	T24490	hypothetical prote
13	32	26.4	97	2	T25754	hypothetical prote
14	32	26.4	249	2	AE1928	hypothetical prote
15	32	26.4	301	2	AE0243	hypothetical prote
16	32	26.4	400	2	T47111	probable acetyl-Co
17	32	26.4	657	2	F97604	hypothetical prote
18	32	26.4	668	2	AH2826	conserved hypothet
19	32	26.4	1017	2	B70985	probable polyketid
20	32	26.4	2774	2	A43359	microtubule-associ
21	31	25.6	159	2	C81662	cytosolic acyl-CoA
22	31	25.6	263	2	C83559	ribonuclease H rnh
23	31	25.6	341	2	T35027	hypothetical prote
24	31	25.6	350	2	AE0637	conserved hypothet
25	31	25.6	358	2	B81194	conserved hypothet
26	31	25.6	358	2	A81831	hypothetical prote
27	31	25.6	392	2	T51772	acetyl-CoA C-acety
28	31	25.6	393	2	C89801	hypothetical prote
29	31	25.6	393	2	S72804	acetyl-CoA C-acety
30	31	25.6	394	2	B48376	acetyl-CoA C-acety
31	31	25.6	395	2	AG2606	conserved hypothet
32	31	25.6	395	2	F97388	probable lipase (A
33	31	25.6	424	2	T14728	probable betaine-a
34	31	25.6	459	2	D34791	interleukin-7 rece
35	31	25.6	504	2	T16526	hypothetical prote
36	31	25.6	518	2	F89888	conserved hypothet
37	31	25.6	558	2	B28392	penicillin amidase
38	31	25.6	558	2	S27199	cephalosporin acyl
39	31	25.6	679	2	T52163	hypothetical prote
40	31	25.6	787	2	T41974	replication origin
41	31	25.6	881	2	RGBYG4	regulatory protein
42	31	25.6	936	2	S57637	hypothetical prote
43	31	25.6	952	2	HXAD5	hexon protein - hu
44	31	25.6	967	1	HXAD2	hexon protein - hu
45	31	25.6	2512	2	E70751	probable nrp prote

ALIGNMENTS

RESULT 1
T12546
hypothetical protein DKFZp586K2120.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
A;Accession: T12546
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17524
A;Molecule type: mRNA
A;Status: preliminary
A;Accession: T12546
A;Residues: 1-1005 <WAM>
A;Cross-references: UNIPROT:Q9H2P0; EMBL:AL080163
A;Experimental source: adult uterus; clone DKFZp586K2120
A;Note: DKFZp586K2120.1

Query Match 33.9%; Score 41; DB 2; Length 1005;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 NAPVSIPQ 48
       ||||||||
Db 257 NAPVSIPQ 264

RESULT 2
B83404
hypothetical protein PA1941 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
A;Accession: B83404
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B
adman, S.; Yuan, Z.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
...; Lory, S.; Olson, M.V.
;Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83404
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-631 <STO>
A;Cross-references: UNIPROT:Q9I2G3; GB:AE004620; GB:AE004091; NID:g9947929; PIDN:AAG053-
A;Experimental source: strain PAO1
C;Genetic:
A;Gene: PA1941

Query Match 29.8%; Score 36; DB 2; Length 631;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      41 NAPVSIPQ 48
           |||||:|||
Db     263 NAPVSYPQ 270
```

RESULT 3
D95412
hypothetical protein SMa2233 [imported] - Sinorhizobium meliloti (strain 1021) megaplasm
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: D95412
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: D95412
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-299 <KUR>
A;Cross-references: UNIPROT:Q92XP0; GB:AE006469; PIDN:AAK65862.1; PID:g14524369; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21362234; PMID:11474104
A;Contents: annotation
A;Genetics:
A;Genome: plasmid

```
Query Match      28.9%;     Score 35;  DB 2;  Length 299;
Best Local Similarity   100.0%;   Pred. No. 14;
Matches   7;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy      42 APVSIPQ 48
           ||||:|||
Db       6 APVSIPQ 12
```

RESULT 4
G69440
conserved hypothetical protein AF1528 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69440
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: G69440
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-136 <KLE>
A;Cross-references: UNIPROT:O28744; GB:AE000997; GB:AE000782; NID:g2689320; PIDN:AAB8972

```
Query Match      28.1%;     Score 34;  DB 2;  Length 136;
Best Local Similarity    75.0%;   Pred. No. 9.3;
Matches   6;   Conservative   1;   Mismatches   1;   Indels   0;   Gaps   0;

Qy      41 NAPVSIPQ 48
           |||:|||
Db      29 NAPFSLPQ 36
```

RESULT 5
T30248
fragile X mental retardation protein 2 - mouse
C;Species: Mus musculus (house mouse)
N;Alternate names: fmr2 protein
R;Chakrabarti, L.; Bristulf, J.; Foss, G.S.; Davies, K.E.
Hum. Mol. Genet. 7, 441-448, 1998
A;Title: Expression of the murine homologue of FMR2 in mouse brain and during developmen
A;Reference number: Z20786; MUID:98133924; PMID:9467002
A;Accession: T30248
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1272 <CHA>
A;Cross-references: UNIPROT:O55112; EMBL:AJ001549; NID:g2832399; PIDN:CAA04821.1; PID:g2
A;Experimental source: brain
C;Genetics:
C;Gene: fmr2
A;Genetics:
A;Gene: fmr2
A;Note: fmr2 expression in an embryo at 11 days is evident to the roof of the hind brain

```
Query Match      28.1%;     Score 34;  DB 2;  Length 1272;
Best Local Similarity    75.0%;   Pred. No. 1.2e+02;
Matches   6;   Conservative   1;   Mismatches   1;   Indels   0;   Gaps   0;

Qy      41 NAPVSIPQ 48
           |||:|||
Db    1191 NGPVTIPQ 1198
```

RESULT 6
AI0632
trp repressor binding protein [imported] - Salmonella enterica subsp. enterica serovar T
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0632
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
th, T.; Connerton, P.; Cronin, A.; Davies, P.; Davis, R.M.; Dowd, L.; White, N.; Farrar,
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0632
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-198 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08244.1; PID:g16502291; GSPDB:GN00176
A;Gene: STY1155
C;Superfamily: trp repressor-binding protein; flavodoxin homology
C;Keywords: flavoprotein

```
Query Match      27.3%;     Score 33;  DB 2;  Length 198;
Best Local Similarity    75.0%;   Pred. No. 23;
Matches   6;   Conservative   1;   Mismatches   1;   Indels   0;   Gaps   0;

Qy      41 NAPVSIPQ 48
           |||||:||
Db      57 NAPAVIPQ 64
```

RESULT 7
AH0813
probable ethanolamine utilization protein EutA eutA [imported] - Salmonella enterica sub
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0813
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
, S.; Moule, S.; O'Gaora, P.; Cronin, A.; Davies, P.; Davis, R.M.; Dowd, L.; White, N.; Farrar,

Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0013
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-467 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07690.1; PID:g16503676; GSPDB:GN00176
C;Genetics:
A;Gene: eutA
C;Superfamily: Escherichia coli hypothetical protein b2451

Qy   41 NAPVSIPQ 48
         ||||||||
Db   338 NLPVAIPQ 345

Query Match   27.3%; Score 33; DB 2; Length 467;
Best Local Similarity   75.0%; Pred. No. 61;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

RESULT 8
H86465
F12G12.1 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86465
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-479 <STO>
A;Cross-references: UNIPROT:Q9FX25; GB:AE005172; NID:g10086460; PIDN:AAG12520.1; GSPDB:G
C;Genetics:
A;Map position: 1

Qy   41 NAPVSIPQ 48
         |||.|:||
Db   226 NAPVNIP 232

Query Match   27.3%; Score 33; DB 2; Length 601;
Best Local Similarity   85.7%; Pred. No. 81;
Matches   6; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

RESULT 9
S47896
probable molybdopterin biosynthesis protein cinnamon - fruit fly (Drosophila melanogaste
C;Species: Drosophila melanogaster
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Jul-2004
C;Accession: S47896
R;Kamdar, K.P.; Shelton, M.E.; Finnerty, V.
Genetics 137, 791-801, 1994
A;Reference number: S47896
A;Title: The Drosophila molybdenum cofactor gene cinnamon is homologous to three Escheri
A;Accession: S47896; MUID:94374679; PMID:8088525
A;Molecule type: mRNA
A;Residues: 1-601 <KAM>
A;Cross-references: EMBL:L19876; NID:g797288; PIDN:AAA65877.1; PID:g505312
C;Genetics:
A;Experimental source: developmental stage embryo
A;Gene: Flybase:cin

C;Cross-references: FlyBase:FBgn0000316
A;Function:
A;Pathway: molybdopterin biosynthesis
C;Superfamily: bifunctional molybdenum cofactor biosynthesis protein, Gephyrin type
C;Keywords: molybdopterin biosynthesis; multifunctional enzyme; transmembrane protein

Qy   41 NAPVSIP 47
         |||||||
Db   226 NAPVNIP 232

RESULT 10
T50995
related to cytoskeleton assembly control protein SlA1 [imported] - Neurospora crassa
N;Alternate names: protein B7F18.140
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Hartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, July 2000
C;Species: Neurospora crassa
A;Accession: T50995
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1119 <SCH>
A;Cross-references: UNIPROT:Q9P3N5; EMBL:AL389891; GSPDB:GN00116; NCSP:B7F18.140
A;Experimental source: BAC clone B7F18; strain OR74A
C;Genetics:
A;Gene: NCSP:B7F18.140
A;Map position: 6
A;Introns: 66/3; 123/2; 495/1

Qy   42 APVSVIPQ 48
         || :|:||
Db   157 APISVPQ 163

Query Match   27.3%; Score 33; DB 2; Length 1119;
Best Local Similarity   71.4%; Pred. No. 1.6e+02;
Matches   5; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

RESULT 11
S16356
ovo protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S16356
R;Mevel-Ninio, M.; Terracol, R.; Kafatos, F.C.
EMBO J. 10, 2259-2266, 1991
A;Title: The ovo gene of Drosophila encodes a zinc finger protein required for female g
A;Reference number: S16356; MUID:91293102; PMID:1712294
A;Accession: S16356
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1213 <MEV>
A;Cross-references: UNIPROT:Q8T8L9; EMBL:X59772
C;Genetics:
A;Gene: FlyBase:ovo
A;Cross-references: FlyBase:FBgn0003028
A;Introns: 931/3; 1152/3

Qy   41 NAPVSIPQ 48
         |:|:|||:
Db   46 NSPISIPK 53

RESULT 12
T24490
hypothetical protein T05A10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24490
R;Sulston, J.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19898
A;Accession: T24490
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2251 <WIL>
A;Cross-references: UNIPROT:Q22190; EMBL:Z68108; PIDN:CAA92133.1; GSPDB:GN00028; CESP:TO
A;Experimental source: clone T05A10
C;Genetics:
A;Gene: CESP:T05A10.1
A;Map position: X
A;Introns: 188/3; 240/3; 420/1; 570/3; 596/1; 732/3; 778/3; 851/3; 1359/2; 1394/2; 1434/

Qy   Query Match   27.3%;   Score 33; DB 2; Length 2251;
            Best Local Similarity   85.7%;   Pred. No. 3.6e+02;
            Matches   6; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIP 47
          ||||:||
Db   1311 NAPVTIP 1317

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <KUR>
A;Cross-references: UNIPROT:Q8YY75; GB:BA000019; PIDN:BAB72933.1; PID:g17130322; GSPDB:G
C;Genetics:
A;Gene: all0976

Qy   Query Match   26.4%;   Score 32; DB 2; Length 249;
            Best Local Similarity   71.4%;   Pred. No. 48;
            Matches   5; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Qy   41 NAPVSIP 47
          |||:|:|
Db   20 NAPLSVP 26

RESULT 15
AE0243
hypothetical protein YP01996 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0243
R;Parkhill, J.; Wren, B. W.; Thomson, N. R.; Titball, R. W.; Holden, M.T.G.; Prentice, M.B
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0243
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <KUR>
A;Cross-references: UNIPROT:Q8ZF00; GB:AL590842; PIDN:CAC90809.1; PID:g15980010; GSPDB:G
C;Genetics:
A;Gene: YP01996

Qy   Query Match   26.4%;   Score 32; DB 2; Length 301;
            Best Local Similarity   85.7%;   Pred. No. 59;
            Matches   6; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   41 NAPVSIP 47
          ||||||
Db   127 NTPVSIP 133

Search completed: February 23, 2005, 19:35:04
Job time : 25.3616 secs

RESULT 13
T25754
hypothetical protein F45E4.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25754
R;Wilson, R.
submitted to the EMBL Data Library, September 1996
A;Description: The sequence of C. elegans cosmid F45E4.
A;Reference number: Z20082
A;Accession: T25754
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-97 <WIL>
A;Cross-references: UNIPROT:Q94228; EMBL:U70852; PIDN:AAB09136.1; GSPDB:GN000022; CESP:F4
A;Experimental source: strain Bristol N2; clone F45E4
C;Genetics:
A;Gene: CESP:F45E4.5
A;Map position: 4
A;Introns: 34/2; 74/1

            Query Match   26.4%;   Score 32; DB 2; Length 97;
            Best Local Similarity   75.0%;   Pred. No. 16;
            Matches   6; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   41 NAPVSIPQ 48
          ||| ||||
Db   18 NAPAPIPQ 25

RESULT 14
AE1928
hypothetical protein all0976 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE1928
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE1928

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: February 23, 2005, 19:09:01 ; Search time 120.175 Seconds
                                             (without alignments)
                                             286.429 Million cell updates/sec

Title: US-09-267-511-3
Perfect score: 120
Sequence: 1 XXXXXXXXXXXXXXXXXXXXXX..........XXXXXXXXXXXXXXXXXX 89
Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5
Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
               1: geneseqp1980s:*
               2: geneseqp1990s:*
               3: geneseqp2000s:*
               4: geneseqp2001s:*
               5: geneseqp2002s:*
               6: geneseqp2003as:*
               7: geneseqp2003bs:*
               8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40	33.3	9	2	AAW64676	Human ADN
2	40	33.3	9	3	AAY71142	Human Act
3	40	33.3	9	3	AAB23471	Activity
4	40	33.3	9	3	AAB23469	Activity
5	40	33.3	9	4	AAB72315	Activity
6	40	33.3	9	5	ABB07215	ADNF I po
7	40	33.3	9	5	ABR39741	ADNF I ac
8	40	33.3	9	7	ADA07952	Human act
9	40	33.3	9	7	ADC16629	Human hea
10	40	33.3	9	8	ADQ76120	ADNF I ac
11	40	33.3	9	8	ADS73608	ADNF I ac
12	40	33.3	10	2	AAW64690	Human ADN
13	40	33.3	10	3	AAY71154	Peptide C
14	40	33.3	10	3	AAB23487	Activity
15	40	33.3	10	4	AAB72321	Activity
16	40	33.3	10	5	ABB07222	ADNF I po
17	40	33.3	10	7	ADA07954	Human act
18	40	33.3	10	8	ADQ76130	ADNF I ac
19	40	33.3	10	8	ADS73615	ADNF I po
20	40	33.3	11	2	AAR94390	Activity
21	40	33.3	11	3	AAB23486	Activity
22	40	33.3	11	4	AAB72327	Activity
23	40	33.3	11	4	AAB72320	Activity
24	40	33.3	11	5	ABB07221	ADNF I po
25	40	33.3	11	8	ADQ76136	ADNF I ac
26	40	33.3	11	8	ADQ76129	ADNF I ac
27	40	33.3	11	8	ADS73630	ADNF I ge
28	40	33.3	11	8	ADS73614	ADNF I po
29	40	33.3	12	3	AAB23485	Activity
30	40	33.3	12	4	AAB72319	Activity
31	40	33.3	12	5	ABB07220	ADNF I po
32	40	33.3	12	8	ADQ76128	ADNF I ac
33	40	33.3	12	8	ADS73613	ADNF I po
34	40	33.3	13	4	AAB23484	Activity
35	40	33.3	13	5	AAB72318	Activity
36	40	33.3	13	8	ABB07219	ADNF I po
37	40	33.3	13	8	ADQ76127	ADNF I ac
38	40	33.3	13	8	ADS73612	ADNF I po
39	40	33.3	14	2	AAR94391	Activity
40	40	33.3	14	2	AAW54057	Activity-
41	40	33.3	14	2	AAY71155	Active pe
42	40	33.3	14	3	AAB23482	Activity
43	40	33.3	14	3	AAY71155	Activity
44	40	33.3	14	4	AAB72316	Activity
45	40	33.3	14	5	ABB07217	ADNF I po

ALIGNMENTS

RESULT 1
AAW64676
ID   AAW64676 standard; protein; 9 AA.
XX
AC   AAW64676;
XX
DT   04-NOV-1998 (first entry)
XX
DE   Human ADNF-III derived active peptide.
XX
KW   Activity dependent neurotrophic factor III; ADNF-III; ADNP; cell death;
KW   activity dependent neuroprotective protein; neurone; excito-toxicity;
KW   spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;
KW   N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
KW   HIV infection.
OS   Homo sapiens.
XX
PN   WO9835042-A2.
XX
PD   13-AUG-1998.
XX
PF   06-FEB-1998; 98WO-US002485.
XX
PR   07-FEB-1997; 97US-0037404P.
XX
PA   (USSH) US SEC HEALTH & HUMAN SERVICES.
XX
PI   Gozes I, Brenneman DE, Bassan M;
XX
DR   WPI; 1998-447233/38.
XX
PT   Activity dependent neurotrophic factor III polypeptide - useful
PT   therapeutically to prevent neuronal cell death associated with e.g. HIV
PT   infection, excito-toxicity or Alzheimer's disease.
XX
PS   Example 4c; Page 67; 121pp; English.
XX
CC   This sequence represents a peptide used in a method which isolates a
CC   novel activity dependent neurotrophic factor III, ADNF-III (also known as
CC   activity dependent neuroprotective protein, ADNP). ADNF III polypeptides
CC   can be used to prevent neuronal cell death, of e.g. the spinal cord,
CC   hippocampal, cerebral cortical or cholinergic neurones associated with
CC   e.g. HIV infection, excito-toxicity induced by N-methyl-D-aspartate
CC   stimulation or beta-amyloid peptide in Alzheimer's disease. The
CC   polypeptides can also be combined with a carrier to alleviate learning
CC   impairment produced by cholinergic blockage in Alzheimer's patients. The
CC   nucleic acids are useful in polypeptide production and to detect ADNF III

CC   polynucleotide in biological samples, while the antibodies are useful
CC   therapeutically and to isolate ADNF III polypeptides
XX
SQ   Sequence 9 AA;

Qy   41 SALLRSIPA 49
             |||||||||
Db   1 SALLRSIPA 9

RESULT 2
AAY71142
ID   AAY71142 standard; peptide; 9 AA.
XX
AC   AAY71142;
XX
DT   08-SEP-2000 (first entry)
XX
DE   Human Activity Dependent Neurotrophic Factor
XX
KW   Activity Dependent Neurotrophic Factor III; ADNF; human; ADNF; ADNF-9;
KW   Activity Dependent Neuroprotective Protein; ADNF III-8 or NAP peptide and;
KW   autosomal dominant nocturnal frontal-lobe epilepsy; neuronal cell death;
KW   neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;
KW   Alzheimer's disease; beta-amyloid peptide; Huntington's disease;
KW   epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;
KW   amyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;
KW   mitochondrial abnormality; Wernicke's encephalopathy; homocysteinuria;
KW   hyperprolinemia; sulphite oxide disease; Tourette's syndrome; nootropic;
KW   Down's syndrome; drug addiction; developmental retardation; antilipemic;
KW   learning impairment; anticonvulsant; neuroprotective; anti-HIV.
XX
OS   Homo sapiens.
XX
PN   WO20002787S-A2.
XX
PD   18-MAY-2000.
XX
PF   04-NOV-1999;   99WO-US026213.
XX
PR   06-NOV-1998;   98US-0018733O.
XX
PA   (USAS) GOVERNMENT US REPRESENT AS.
PA   (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX
PI   Gozes I, Brenneman DE, Bassan M, Zamostiano R;
XX
XX
DR   WPI; 2000-376491/32.
XX
PT   New nucleic acid encoding an activity dependent neurotrophic factor III
PT   (ADNF III) useful in the treatment of neurological deficiencies and for
PT   preventing neuronal cell death.
XX
PS   Example; Page 5; 136pp; English.
XX
XX
CC   The present sequence is the human Activity Dependent Neurotrophic Factor
CC   (ADNF)-9 active peptide sequence. The ADNF III-8 or NAP peptide was
CC   synthesised based on the structural homology to cloned ADNF III. ADNF III
CC   is also used for immunological detection of cloned ADNF III. ADNF III
CC   is also called an Activity Dependent Neuroprotective Protein (ADNP). The
CC   human gene was mapped to chromosome 20q13.2 and is linked to autosomal
CC   dominant nocturnal frontal-lobe epilepsy (ADNFLE) gene. It is expressed
CC   in the astrocytes, brain and also in foetal lung and endocrine tissues.
CC   This sequence has homology to ADNF I and hsp60, heat shock protein and
CC   PIFI, a DNA repair protein. The ADNF III polypeptides are useful for the
CC   treatment of neurological deficiencies and for prevention of neuronal
CC   cell death associated with gp120, the envelope protein from HIV; N-methyl
CC   -D-Aspartic acid (excito-toxicity); tetrodotoxin (blockage of electrical
CC   activity); and beta-amyloid peptide, a substance related to neuronal

---

CC   degeneration in Alzheimer's disease. It is useful for the treatment of
CC   Huntington's disease, AIDS dementia complex, epilepsy, neuropathic pain
CC   syndromes, Parkinson's disease, amyotrophic lateral sclerosis (ALS),
CC   mitochondrial abnormalities, Leber's disease, Wernicke's encephalopathy,
CC   Alzheimer's disease, homocysteinuria, hyperprolinemia, sulphite oxide
CC   disease, Tourette's syndrome, oxidative stress induced neuronal death,
CC   Down's syndrome, developmental retardation and learning impairments, drug
CC   addiction, tolerance and dependency
XX
SQ   Sequence 9 AA;

Qy   41 SALLRSIPA 49
             |||||||||
Db   1 SALLRSIPA 9

Query Match   33.3%; Score 40; DB 2; Length 9;
Best Local Similarity   100.0%;   Pred. No. 1.8e+06;
  Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 3
AAB23471
ID   AAB23471 standard; peptide; 9 AA.
XX
AC   AAB23471;
XX
DT   22-JAN-2001 (first entry)
XX
DE   Activity dependent neurotrophic factor I peptide #3.
XX
KW   Activity dependent neurotrophic factor; ADNF; FAS;
KW   foetal alcohol syndrome; gene therapy; neurological deficiency;
KW   neuronal cell death.
XX
OS   Unidentified.
XX
PN   WO200053217-A2.
XX
PD   14-SEP-2000.
XX
PF   10-MAR-2000; 2000WO-US006364.
XX
PR   12-MAR-1999;   99US-0026751I.
XX
PA   (UYRA-) UNIV RAMOT.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Brenneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;
XX
XX
DR   WPI; 2000-601940/57.
XX
PT   Treating condition associated with fetal alcohol syndrome in a subject
PT   exposed to alcohol in utero or reducing neuronal death, involves
PT   administering activity dependent neurotrophic factors I and/or III.
XX
PS   Disclosure; Page 51; 65pp; English.
XX
CC   The present invention relates to the treatment of a condition associated
CC   with foetal alcohol syndrome (FAS), involving administering an activity
CC   dependent neurotropic factor (ADNF). ADNFs of the present invention may
CC   also be used to treat neurological deficiencies and prevent neuronal cell
CC   death. The present sequence is an ADNF peptide
XX
SQ   Sequence 9 AA;

Qy   41 SALLRSIPA 49
             |||||||||
Db   1 SALLRSIPA 9

Query Match   33.3%; Score 40; DB 3; Length 9;
Best Local Similarity   100.0%;   Pred. No. 1.8e+06;
  Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 4
AAB23469
ID   AAB23469 standard; peptide; 9 AA.
XX
AC   AAB23469;
XX
DT   22-JAN-2001 (first entry)
XX
DE   Activity dependent neurotrophic factor I peptide #1.
XX
KW   Activity dependent neurotrophic factor; ADNF; FAS;
KW   foetal alcohol syndrome; gene therapy; neurological deficiency;
KW   neuronal cell death.
XX
OS   Unidentified.
XX
PN   WO200053217-A2.
XX
PD   14-SEP-2000.
XX
PF   10-MAR-2000; 2000WO-US006364.
XX
PR   12-MAR-1999; 99US-00267511.
XX
PA   (UYRA-) UNIV RAMOT.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Brenneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;
XX
DR   WPI; 2000-601940/57.
XX
PT   Treating condition associated with fetal alcohol syndrome in a subject
PT   exposed to alcohol in utero or reducing neurological deficiencies and
PT   administering activity dependent neurotrophic factors I and/or III.
XX
PS   Claim 5; Page 51; 65pp; English.
XX
CC   The present invention relates to the treatment of a condition associated
CC   with foetal alcohol syndrome (FAS), involving administering an activity
CC   dependent neurotropic factor (ADNF). ADNFs of the present invention may
CC   also be used to treat neurological deficiencies and prevent neuronal cell
CC   death. The present sequence is an ADNF peptide
XX
SQ   Sequence 9 AA;

Qy   41 SALLRSIPA 49
        |||||||||
Db   1 SALLRSIPA 9

Query Match   33.3%; Score 40; DB 3; Length 9 ;
Best Local Similarity   100.0%; Pred. No. 1.8e+06;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 5
AAB72315
ID   AAB72315 standard; peptide; 9 AA.
XX
AC   AAB72315;
XX
DT   16-MAY-2001 (first entry)
XX
DE   Activity dependent neurotrophic factor I (ADNF I) peptide SEQ ID 1.
XX
KW   Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;
KW   neuronal cell death; Alzheimer's disease; oxidative stress; VIP;
KW   vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.
XX
OS   Synthetic.
XX
PN   WO200112654-A2.

PD   22-FEB-2001.
XX
PF   17-AUG-2000; 2000WO-US022861.
XX
PR   18-AUG-1999; 99US-0149956P.
XX
PA   (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Brenneman DE, Gozes I, Spong CY, Pinhasov A, Giladi E;
XX
DR   WPI; 2001-202855/20.
XX
PT   Novel Activity Dependent Neurotrophic Factor I useful for treating
PT   oxidative stress, reducing neuronal cell death and treating a condition
PT   associated with fetal alcohol syndrome.
XX
PS   Claim 2; Page 56; 88pp; English.
XX
CC   This invention relates to an activity dependent neurotrophic factor I
CC   (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72321 represent
CC   ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent
CC   ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical
CC   composition containing either ADNF I or ADNF III are useful for reducing
CC   neuronal cell death, e.g. death of spinal cord neurons, hippocampal
CC   neurons, cerebral cortical neurons and cholinergic neurons, in a patient
CC   infected with a virus, e.g. human immunodeficiency virus (HIV). The
CC   neuronal cell death is associated with excito-toxicity induced by N-
CC   methyl-D-aspartate (NMDE) stimulation, which is induced by beta-amyloid
CC   peptide in an Alzheimer's disease patient, or induced by cholinergic
CC   blockade. ADNF I, ADNF III and the pharmaceutical composition are also
CC   useful for treating oxidative stress in a patient, for reducing a
CC   condition, such as decreased body weight, decreased brain weight,
CC   decreased level of vasoactive intestinal peptide (VIP) mRNA, and foetal
CC   death, associated with foetal alcohol syndrome
XX
SQ   Sequence 9 AA;

Qy   41 SALLRSIPA 49
        |||||||||
Db   1 SALLRSIPA 9

Query Match   33.3%; Score 40; DB 4; Length 9 ;
Best Local Similarity   100.0%; Pred. No. 1.8e+06;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 6
ABB07215
ID   ABB07215 standard; peptide; 9 AA.
XX
AC   ABB07215;
XX
DT   26-MAR-2002 (first entry)
XX
DE   ADNF I polypeptide active core site peptide sequence.
XX
KW   ADNF; Activity Dependent Neurotrophic Factor; nootropic; neuroprotective;
KW   cerebroprotective; antidiabetic; neuroleptic; anticonvulsant; anti-HIV;
KW   antiparkinsonian; tranquilizer; antialcoholic; vulnerary; antibacterial;
KW   antiinflammatory; antidote; ophthalmological; muscular; vasodilator;
KW   NMDA receptor.
XX
OS   Synthetic.
XX
PN   WO200192333-A2.
XX
PD   06-DEC-2001.
XX
PF   31-MAY-2001; 2001WO-US017758.
XX
PR   31-MAY-2000; 2000US-0208944P.
PR   08-FEB-2001; 2001US-0267805P.

```
XX
PA  (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Spong CY, Brenneman D, Gozes I;
XX
DR  WPI; 2002-114330/15.
XX
PT  Use of an activity dependent neurotropic factor for improving learning
PT  and/or memory in a subject by pre- or post-natal administration.
XX
PS  Claim 1; Page 51; 80pp; English.
XX
CC  The invention provides a method of improving learning and/or memory in a
CC  subject that involves administering pre- or postnatally an Activity
CC  Dependent Neurotrophic Factor (ADNF) to the subject. The ADNF polypeptide
CC  is an ADNF I and/or an ADNF III polypeptide comprising the core active
CC  site sequences ABB07215 or ABB07216. The method is useful for improving
CC  learning and/or memory in a subject; for treating a normal or old subject
CC  afflicted with neuropathology, Alzheimer's disease, Down's syndrome, a
CC  normal mental capacity, mental retardation, for the treatment of central
CC  motor systems including degenerative conditions affecting the basal
CC  ganglia (such as Huntington's disease, Wilson's disease, striatonigral
CC  degeneration, corticobasal ganglionic degeneration), Tourette's syndrome,
CC  Parkinson's disease, progressive supranuclear palsy, progressive bulbar
CC  palsy, familial spastic paraplegia, spinomuscular atrophy, dentatorubral
CC  atrophy, olivo-pontocerebellar atrophy, paraneoplastic cerebellar
CC  degeneration, dopamine toxicity, diseases affecting sensory neurons such
CC  as Friedreich's ataxia, diabetes, peripheral neuropathy, retinal neuronal
CC  degeneration; diseases of limbic and cortical systems such as cerebral
CC  amyloidosis, Pick's atrophy, Retts syndrome; neurodegenerative
CC  pathologies involving multiple neuronal systems and/or brainstem
CC  including AIDS-related dementia, Leigh's disease, diffuse Lewy body
CC  disease, epilepsy, multiple system atrophy, Guillain-barre syndrome,
CC  lysosomal storage disorders such as lipofuscinosis, late-degenerative
CC  stages of Down's syndrome, Alper's disease, vertigo as a result of CNS
CC  degeneration; pathologies associated with developmental retardation and
CC  learning impairments, oxidative stress induced neuronal death;
CC  pathologies arising with aging and chronic alcohol or drug abuse
CC  including for e.g. with alcoholism the degeneration of neurons in locus
CC  coeruleus, cerebellum, cholinergic basal forebrain; with aging
CC  degeneration of cerebellar neurons and cortical neurons leading to
CC  cognitive and motor impairments; with chronic amphetamine abuse
CC  degeneration of basal ganglia neurons leading to motor impairments;
CC  pathological changes resulting from focal trauma such as stroke, focal
CC  ischemia, vascular insufficiency, hypoxic-ischemia encephalopathy,
CC  hyperglycemia, hypoglycemia, closed head trauma or direct trauma. The
CC  present sequence represents the active core site sequence of the ADNF I
CC  polypeptide
XX
SQ  Sequence 9 AA;
XX
Qy  41 SALLRSIPA 49
       |||||||||
Db   1 SALLRSIPA 9

Query Match        33.3%;  Score 40;  DB 5;  Length 9;
Best Local Similarity  100.0%;  Pred. No. 1.8e+06;
Matches  9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

```
RESULT 7
ABR39741
ID   ABR39741 standard; peptide; 9 AA.
XX
AC   ABR39741;
XX
DT   23-JUN-2003  (first entry)
XX
DE   ADNF I active core peptide fragment SAL.
XX
KW   ADNF I; Activity Dependent Neurotrophic Factor I; neuroprotective;
KW   anti-HIV; neuroleptic; antiparkinsonian; nootropic; ADNF-9; SAL.
```

```
XX
OS   Unidentified.
XX
PN   WO200302226-A2.
XX
XX
PD   20-MAR-2003.
XX
PF   12-SEP-2002; 2002WO-US029146.
XX
PR   12-SEP-2001; 2001US-0322760P.
PR   10-APR-2002; 2002US-03719961P.
XX
DR   WPI; 2003-354501/33.
XX
PI   Brenneman DE, Castellon R, Spong CY, Hauser JM, Gozes I;
XX
PA   (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PS   Disclosure; Page 2; 111pp; English.
XX
PT   New Activity Dependent Neurotrophic Factor I complex polypeptide, useful
PT   for reducing neuronal cell death, treating oxidative stress in a patient,
PT   or improving learning and/or memory in a subject with e.g. Alzheimer's
PT   disease.
XX
CC   The invention relates to Activity Dependent Neurotrophic Factor I (ADNF
CC   I) complex polypeptide selected from sequences ABR39744-754. The ADNF I
CC   complex polypeptide is useful for reducing neuronal cell death in
CC   conditions such as HIV infection, treating oxidative stress in a patient,
CC   reducing a condition associated with fetal alcohol syndrome, or improving
CC   learning and/or memory in a subject with e.g. Alzheimer's disease or
CC   Down's syndrome. The ADNF complex polypeptides are also useful in
CC   designing a drug treatment regime that can be individually tailored for
CC   each patient affected by neurodegenerative disorders. The polypeptides
CC   can also be used for diagnosing or treating Huntington's disease,
CC   Wilson's disease, Parkinson's disease, AIDS-related dementia or
CC   Tourette's syndrome. The present sequence represents a peptide that
CC   captured the survival-promoting activity of ADNF I, and is designated
CC   ADNF-9 or SAL.
XX
SQ   Sequence 9 AA;
XX
Qy   41 SALLRSIPA 49
        |||||||||
Db    1 SALLRSIPA 9

Query Match        33.3%;  Score 40;  DB 6;  Length 9;
Best Local Similarity  100.0%;  Pred. No. 1.8e+06;
Matches  9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

```
RESULT 8
ADA07952
ID   ADA07952 standard; peptide; 9 AA.
XX
AC   ADA07952;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human activity dependent neuroprotective factor (ADNP) peptide #1.
XX
OS   Homo sapiens.
XX
PN   US2003166544-A1.
XX
KW   Human; glaucomatous optic neuropathy;
KW   activity dependent neuroprotective factor; ADNP; ophthalmological.
XX
PD   04-SEP-2003.
XX
PF   06-JUN-2002; 2002US-00164432.
XX
```

PR   07-SEP-2000; 2000US-0230964P.
PR   02-AUG-2001; 2001US-00921029.
XX
PA   (CLAR/) CLARK A F.
PA   (SHAD/) SHADE D L.
XX
PI   Clark AF, Shade DL;
XX
DR   WPI; 2003-720933/68.
XX
PT   Treating glaucomatous optic neuropathy by administering a composition
PT   comprising a peptide derived from or related to Activity Dependent
PT   Neuroprotective Factor (ADNP).
XX
PS   Claim 5; Page 2; 13pp; English.
XX
CC   The present invention relates to a method for preventing and treating
CC   glaucomatous optic neuropathy. The method comprises administering a
CC   composition comprising a peptide derived from activity dependent
CC   neuroprotective factor (ADNP). The method is useful for treating
CC   glaucomatous optic neuropathy. The present sequence represents a peptide
CC   from human ADNP.
XX
SQ   Sequence 9 AA;

Query Match   33.3%; Score 40; DB 7; Length 9;
Best Local Similarity   100.0%;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 SALLRSIPA 49
               |||||||||
Db   1 SALLRSIPA 9

RESULT 9
ADC16629
ID   ADC16629 standard; peptide; 9 AA.
XX
AC   ADC16629;
XX
DT   18-DEC-2003 (first entry)
XX
DE   Human heat shock protein 60 peptide p277 analogue Seq ID7.
XX
KW   heat shock protein; Hsp; antigen presenting cell; dendritic cell; T cell;
KW   immunomodulatory cytokine; cytokine; chemokine; surface antigen;
KW   parasitic disease; inflammatory disease; autoimmune disease;
KW   graft rejection; cancer; allergy; Hsp60; antiinflammatory;
KW   immunosuppressive; antiparasitic; cytostatic; antiallergic;
KW   human; p277(442-450, Ser6Ser11).
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO200063759-A2.
XX
PD   07-AUG-2003.
XX
PF   30-JAN-2003; 2003WO-IL000078.
PR   31-JAN-2002; 2002US-0352594P.
XX
PA   (PEPT-) PEPTOR LTD.
XX
PI   Karmon Y, Avron A, Elias D;
XX
DR   WPI; 2003-663414/62.
XX
PT   Identifying a heat shock protein (Hsp) derived peptide for diagnosing or
PT   treating e.g. cancer by comparing the amount of cytokines produced by T
PT   cells exposed to antigen presenting cells not previously exposed to the
PT   test peptide.
XX

Claim 23; SEQ ID NO 7; 47pp; English.
XX
CC   This invention relates to a novel heat shock protein (Hsp) derived
CC   peptide for use in diagnosis or therapy. Exposure of antigen presenting
CC   cells, particularly dendritic cells, to peptides or peptide analogues
CC   derived from heat shock proteins subsequently activates T cells to
CC   produce immunomodulatory cytokines and will directly influence the
CC   cytokines, chemokines and surface antigens produced by the exposed
CC   antigen presenting cells. The present invention provides peptides and
CC   peptide analogues of heat shock proteins capable of directly interacting
CC   with dendritic cells. The peptides of the invention may be useful for the
CC   treatment of parasitic, inflammatory or autoimmune disease or graft
CC   rejection, cancer or allergy. The preferred peptides of the invention are
CC   peptide fragments (p277) or analogues (of p277), derived from heat shock
CC   protein Hsp60. They may have antiinflammatory, immunosuppressive,
CC   antiparasitic, cytostatic or antiallergic activities. The present
CC   sequences of the invention may also be useful for gene therapy. The
CC   present sequence is the amino acid sequence of human heat shock protein
CC   (Hsp) 60 peptide fragment p277 analogue p277 (442-450, Ser6Ser11) of the
CC   invention.
XX
SQ   Sequence 9 AA;

Query Match   33.3%; Score 40; DB 7; Length 9;
Best Local Similarity   100.0%;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 SALLRSIPA 49
               |||||||||
Db   1 SALLRSIPA 9

RESULT 10
ADQ76120
ID   ADQ76120 standard; peptide; 9 AA.
XX
AC   ADQ76120;
XX
DT   07-OCT-2004 (first entry)
XX
DE   ADNF I active core site peptide SEQ ID NO.1.
XX
KW   activity dependent neurotropic factor; ADNF; ADNF I; active core site;
KW   immunosuppressive; nootropic; neuroprotective; antiinflammatory;
KW   vasotropic; muscular; CNS; thyromimetic; antithyroid; antirheumatic;
KW   antiarthritic; hepatotropic; virucide; dermatological; haemostatic;
KW   antidiabetic; antibacterial; neurotropic factor agonist;
KW   autoimmune disease; multiple sclerosis; myasthenia gravis;
KW   Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;
KW   Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;
KW   hypothyroiditis; primary biliary cirrhosis;
KW   mixed connective tissue disease; chronic active hepatitis;
KW   Graves' disease; hyperthyroiditis; scleroderma;
KW   chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;
KW   septic shock.
XX
OS   Synthetic.
XX
PN   WO2004060309-A2.
XX
PD   22-JUL-2004.
XX
PF   30-DEC-2003; 2003WO-US041540.
PR   02-JAN-2003; 2003US-0437650P.
XX
PA   (UTRA-) UNIV RAMOT AT TEL AVIV LTD.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Gozes I, Offen D, Giladi E, Melamed E, Brenneman D;
XX
DR   WPI; 2004-543782/52.
XX

RESULT 11

```
ID   ADS73608 standard; peptide; 9 AA.
XX
AC   ADS73608;
XX
DT   16-DEC-2004  (first entry)
XX
DE   ADNF I active core site.
XX
KW   active ; core peptide ; Activity Dependent Neurotropic Factor ; ADNF;
KW   ADNF I; ADNF III; anxiety ; depression ; lipophilic moiety ;
KW   penetration; activity; panic disorder; obsessive-compulsive disorder;
KW   post-traumatic stress disorder; social phobia; social anxiety disorder;
KW   specific phobia; generalized anxiety disorder; Major depression;
KW   dysthymia; bipolar disorder; NAP-tubulin ; binding site; anxiolytic drug;
KW   neuroprotection.
XX
OS   Homo sapiens.
XX
PN   WO2004080957-A2.
XX
PD   23-SEP-2004.
XX
PF   11-MAR-2004; 2004WO-IL000232.
PR   12-MAR-2003; 2003US-0454505P.
PA   (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
XX
PT   Preventing or treating autoimmune diseases, such as multiple sclerosis,
PT   rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic
     shock, using an Activity Dependent Neurotropic Factor (ADNF) polypeptide.
XX
PS   Claim 1; SEQ ID NO 1; 39pp; English.
XX
CC   The present invention describes a method for preventing or treating an
CC   autoimmune disease in a subject. The method comprises administering an
CC   activity dependent neurotropic factor (ADNF) polypeptide, where the ADNF
CC   polypeptide is a member selected from the group consisting of: (a) an
CC   ADNF I polypeptide comprising an active core site with the amino acid
CC   sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide
CC   comprising an active core site with the amino acid sequence of SEQ ID
CC   NO:2 (ADQ76121); and (c) a mixture of part (a)
CC   and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
CC   host cells, vectors and antibodies used in the methods are also disclosed
CC   in the present invention. ADNF sequences have immunosuppressive,
CC   nootropic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
CC   thyromimetic, antithyroid, antirheumatic, antiarthritic, hepatotropic,
CC   virucide, dermatological, haemostatic, antidiabetic and antibacterial
CC   activities, and can be used as neurotropic factor agonists. The methods
CC   and compositions of the present invention are useful for the prevention
CC   and/or treatment of autoimmune diseases, such as multiple sclerosis,
CC   myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,
CC   Behcet's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
CC   disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
CC   tissue disease, chronic active hepatitis, Graves'
CC   disease/hyperthyroiditis, scleroderma, chronic idiopathic
CC   thrombocytopenic purpura, diabetic neuropathy and septic shock. The
CC   present sequence represents an ADNF I active core site peptide from the
CC   present invention.
XX
SQ   Sequence 9 AA;
```

```
Qy          41 SALLRSIPA 49
               |||||||||
Db           1 SALLRSIPA 9
```

```
Query Match             33.3%;  Score 40;  DB 8;  Length 9;
Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

RESULT 12

```
ID   AAW64690 standard; protein; 10 AA.
XX
AC   AAW64690;
XX
DT   04-NOV-1998  (first entry)
XX
DE   Human ADNF-III antigenic peptide.
XX
KW   Activity dependent neurotrophic factor III; ADNF-III; ADNP; cell death;
KW   activity dependent neuroprotective protein; neurone; excito-toxicity;
KW   spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;
KW   N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
KW   HIV infection.
XX
OS   Synthetic.
XX
PN   WO9835042-A2.
XX
PD   13-AUG-1998.
XX
PF   06-FEB-1998; 98WO-US002485.
XX
PR   07-FEB-1997; 97US-0037404P.
XX
PA   (USSH ) US SEC HEALTH & HUMAN SERVICES.
XX
PI   Gozes I, Brenneman DE, Bassan M;
XX
     WPI; 1998-447239/38.
XX
PT   Activity dependent neurotrophic factor III polypeptide - useful
PT   therapeutically to prevent neuronal cell death associated with e.g. HIV
     infection, excito-toxicity or Alzheimer's disease.
XX
PS   Example 4b; Page 67; 121pp; English.
```

```
PI   Gozes I, Alcalay RN, Divinski I, Giladi E;
XX
     WPI; 2004-668930/65.
XX
PT   Treating or preventing anxiety or depression in a subject comprises
PT   administering an amount of an Activity Dependent Neurotropic Factor
     polypeptide to the subject.
XX
PS   Claim 2; SEQ ID NO 1; 46pp; English.
XX
CC   This sequence represents the active core peptide derived from Activity
CC   Dependent Neurotrophic Factor (ADNF) I. This peptide may be used for
CC   treating or preventing anxiety or depression in a subject. This sequence
CC   may optionally be extended at either the N- and/or the C-terminals. The
CC   ADNF polypeptide of the invention may be encoded by a nucleic acid that
CC   is administered to the subject. It also contains a covalently bound
CC   lipophilic moiety to enhance penetration or activity. The subject suffers
CC   from anxiety or depression and the ADNF polypeptide is administered to
CC   prevent anxiety or depression. The disease is selected from a panic
CC   disorder, obsessive-compulsive disorder, post-traumatic stress disorder,
CC   social phobia, social anxiety disorder, specific phobias, generalized
CC   anxiety disorder, Major depression, dysthymia, and bipolar disorder. The
CC   NAP-tubulin binding site(s) is/are used to identify anxiolytic drugs and
CC   drugs that alleviate depression and provide neuroprotection.
XX
SQ   Sequence 9 AA;
```

```
Qy          41 SALLRSIPA 49
               |||||||||
Db           1 SALLRSIPA 9
```

```
Query Match             33.3%;  Score 40;  DB 8;  Length 9;
Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

XX
CC   This sequence represents a peptide used in a method which isolates a
CC   novel activity dependent neurotrophic factor III, ADNF-III (also known as
CC   activity dependent neuroprotective protein, ADNP). ADNF III polypeptides
CC   can be used to prevent neuronal cell death, of e.g. the spinal cord,
CC   hippocampal, cerebral cortical or cholinergic neurones associated with
CC   e.g. HIV infection, excito-toxicity induced by N-methyl-D-aspartate
CC   stimulation or beta-amyloid peptide in Alzheimer's disease. The
CC   polypeptides can also be combined with a carrier to alleviate learning
CC   impairment produced by cholinergic blockage in Alzheimer's patients. The
CC   nucleic acids are useful in polypeptide production and to detect ADNF III
CC   polynucleotide in biological samples, while the antibodies are useful
CC   therapeutically and to isolate ADNF III polypeptides
XX
SQ   Sequence 10 AA;

Qy   Query Match   33.3%; Score 40; DB 2; Length 10;
     Best Local Similarity   100.0%; Pred. No. 0.092;
     Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   41 SALLRSIPA 49
              |||||||||
Db   2 SALLRSIPA 10

RESULT 13
AAY71154
ID   AAY71154 standard; peptide; 10 AA.
AC   AAY71154;
XX
DT   08-SEP-2000 (first entry)
XX
DE   Peptide CSALLRSIPA used for affinity column chromatography.
XX
KW   Activity Dependent Neurotrophic Factor III; ADNF; chromosome 20q13.2;
KW   Activity Dependent Neuroprotective Protein; ADNP; neuronal cell death;
KW   autosomal dominant nocturnal frontal-lobe epilepsy; ADNFLE;
KW   neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;
KW   Alzheimer's disease; beta-amyloid peptide; Huntington's disease;
KW   epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;
KW   amyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;
KW   mitochondrial abnormality; Wernicke's encephalopathy; homocysteinuria;
KW   hyperprolinemia; sulphite oxide disease; Tourette's syndrome; nootropic;
KW   Down's syndrome; drug addiction; developmental retardation; antilipemic;
KW   learning impairment; anticonvulsant; neuroprotective; anti-HIV.
XX
OS   Unidentified.
XX
PN   WO200027875-A2.
XX
PD   18-MAY-2000.
XX
PF   04-NOV-1999; 99WO-US026213.
XX
PR   06-NOV-1998; 98US-0187330.
XX
PA   (USAS) GOVERNMENT US REPRESENT AS.
PA   (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX
PI   Gozes I, Brenneman DE, Bassan M, Zamostiano R;
XX
DR   WPI; 2000-376491/32.
XX
PT   New nucleic acid encoding an activity dependent neurotrophic factor III
PT   (ADNF III) useful in the treatment of neurological deficiencies and for
PT   preventing neuronal cell death.
XX
PS   Example; Page 71; 136pp; English.
XX
CC   The present peptide sequence is used for affinity column chromatography,
CC   for purification of antibodies to Activity Dependent Neurotrophic Factor
CC   (ADNF), also called an Activity Dependent Neuroprotective Protein (ADNP).

CC   The human gene is mapped to chromosome 20q13.2 and is linked to autosomal
CC   dominant nocturnal frontal-lobe epilepsy (ADNFLE) gene. It is expressed
CC   in the astrocytes, brain and also in foetal lung and endocrine tissues.
CC   This sequence has homology to ADNF I and hsp60, heat shock protein and
CC   PIF1, a DNA repair protein. The ADNF III polypeptides are useful for the
CC   treatment of neurological deficiencies and for prevention of neuronal
CC   cell death associated with gp120, the envelope protein from HIV; N-methyl
CC   -D-Aspartic acid (excito-toxicity); tetrodotoxin (blockage of electrical
CC   activity); and beta-amyloid peptide, a substance related to neuronal
CC   degeneration in Alzheimer's disease. It is useful for the treatment of
CC   Huntington's disease, AIDS dementia complex, epilepsy, neuropathic pain
CC   syndromes, Parkinson's disease, amyotrophic lateral sclerosis (ALS),
CC   mitochondrial abnormalities, Leber's disease, Wernicke's encephalopathy,
CC   Alzheimer's disease, homocysteinuria, hyperprolinemia, sulphite oxide
CC   disease, Tourette's syndrome, oxidative stress induced neuronal death,
CC   Down's syndrome, developmental retardation and learning impairment, drug
CC   addiction, tolerance and dependency
XX
SQ   Sequence 10 AA;

Qy   Query Match   33.3%; Score 40; DB 3; Length 10;
     Best Local Similarity   100.0%; Pred. No. 0.092;
     Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   41 SALLRSIPA 49
              |||||||||
Db   2 SALLRSIPA 10

RESULT 14
AAB23487
ID   AAB23487 standard; peptide; 10 AA.
AC   AAB23487;
XX
DT   14-MAY-2003 (revised)
DT   22-JAN-2001 (first entry)
XX
DE   Activity dependent neurotrophic factor I peptide #19.
XX
KW   Activity dependent neurotrophic factor; ADNF; FAS;
KW   foetal alcohol syndrome; gene therapy; neurological deficiency;
KW   neuronal cell death.
XX
OS   Unidentified.
XX
PN   WO200053217-A2.
XX
PD   14-SEP-2000.
XX
PF   10-MAR-2000; 2000WO-US006364.
XX
PR   12-MAR-1999; 99US-0267511.
XX
PA   (UYRA-) UNIV RAMOT;
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Brenneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;
XX
DR   WPI; 2000-601940/57.
XX
PT   Treating condition associated with fetal alcohol syndrome in a subject
PT   exposed to alcohol in utero or reducing neuronal death, involves
PT   administering activity dependent neurotrophic factors I and/or III.
XX
PS   Claim 6; Page 4; 65pp; English.
XX
CC   The present invention relates to the treatment of a condition associated
CC   with foetal alcohol syndrome (FAS); involving administering an activity
CC   dependent neurotrophic factor (ADNF). ADNFs of the present invention may
CC   also be used to treat neurological deficiencies and prevent neuronal cell
CC   death. The present sequence is an ADNF peptide. (Updated on 14-MAY-2003
CC   to correct PS field.)

```
XX
SQ   Sequence 10 AA;

     Query Match           33.3%;    Score 40;  DB 3;  Length 10;
     Best Local Similarity 100.0%;   Pred. No. 0.092;
     Matches    9;   Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      41 SALLRSIPA 49
            |||||||||
Db       2 SALLRSIPA 10


RESULT 15
AAB72321
ID   AAB72321 standard; peptide; 10 AA.
XX
AC   AAB72321;
XX
DT   16-MAY-2001  (first entry)
XX
DE   Activity dependent neurotrophic factor I (ADNF I) peptide SEQ ID 19.
XX
KW   Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;
KW   neuronal cell death; Alzheimer's disease; oxidative stress; VIP;
KW   vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.
XX
OS   Synthetic.
XX
PN   WO20011265_4-A2.
XX
PD   22-FEB-2001.
XX
PF   17-AUG-2000; 2000WO-US022861.
XX
PR   18-AUG-1999;    99US-0149956P.
XX
PI   Brenneman DE,  Gozes I,  Spong CY,  Pinhasov A,  Giladi E;
XX
PA   (UYRA-)  UNIV RAMOT APPLIED RES & IND DEV LTD.
PA   (USSH )  US DEPT HEALTH & HUMAN SERVICES.
XX
DR   WPI; 2001-202855/20.
XX
PT   Novel Activity Dependent Neurotrophic Factor I useful for treating
PT   oxidative stress, reducing neuronal cell death and treating a condition
PT   associated with fetal alcohol syndrome.
XX
PS   Claim 7; Page 56; 88pp; English.
XX
CC   This invention relates to an activity dependent neurotrophic factor I
CC   (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72321 represent
CC   ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent
CC   ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical
CC   composition containing either ADNF I or ADNF III are useful for reducing
CC   neuronal cell death, e.g. death of spinal cord neurons, hippocampal
CC   neurons, cerebral cortical neurons and cholinergic neurons, in a patient
CC   infected with a virus, e.g. human immunodeficiency virus (HIV). The
CC   neuronal cell death is associated with excito-toxicity induced by N-
CC   methyl-D-aspartate (NMDE) stimulation, which is induced by beta-amyloid
CC   peptide in an Alzheimer's disease patient, or induced by cholinergic
CC   blockade. ADNF I, ADNF III and the pharmaceutical composition are also
CC   useful for treating oxidative stress in a patient, for reducing a
CC   condition, such as decreased body weight, decreased brain weight,
CC   decreased level of vasoactive intestinal peptide (VIP) mRNA, and foetal
CC   death, associated with foetal alcohol syndrome.
XX
SQ   Sequence 10 AA;

     Query Match           33.3%;    Score 40;  DB 4;  Length 10;
     Best Local Similarity 100.0%;   Pred. No. 0.092;
     Matches    9;   Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      41 SALLRSIPA 49
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Db   2 SALLRSIPA 10

Db   2 ||||||||| SALLRSIPA 10

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